
UVI LIGHT

XTD

User's manual

Version: A



SCHOTT
Instruments

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1 REMARKS

2 WARRANTY

The new equipment and material sold by SCHOTT INSTRUMENTS is guaranteed against any manufacturing defects for one year (unless otherwise stated by SCHOTT INSTRUMENTS) with effect :

- From the technical acceptance of the equipment in the factory by the buyer or his designee,
- or failing this :
 - * For Metropolitan France: from the date on the delivery note.
 - * For other destinations: from the date of factory shipment certified by air waybill, consignment note or bill of lading.

The SCHOTT INSTRUMENTS company guarantee applies exclusively to defectiveness arising from a design fault or from a concealed defect. It is strictly limited to the free dispatching of replacement parts (except for consumable items) or to the repairing of the equipment in our workshops within a deadline of 10 working days (shipping delay not included).

By express agreement, the following are strictly excluded from our guarantee:

- All damages, notably for staff costs, loss of earnings, business trouble, etc
- Any breakdown due to an incorrect use of the equipment (non adapted mains, fall, attempt at transformation, etc) or to a lack of maintenance by the user or to poor storage conditions.
- Any breakdown due to the use of parts not supplied by SCHOTT INSTRUMENTS, on SCHOTT INSTRUMENTS equipment
- Any breakdown due to the transporting of the equipment in packaging which is not its original packaging
- The lamps, the cells and generally any item which appears in the "accessories" section on the price list.

Our customers are kindly asked to apply for our consent before returning any instrument for repair. No return of materials may be accepted without the prior written consent of our Sales Management which will precise the terms of such return.

If the above consent is given, articles shall be returned in their original packaging on a prepaid basis to the following address:

SCHOTT-INSTRUMENTS Hattenbergstraße 10 55122 Mainz, Germany

We reserve the right to reship all instruments received collect failing such consent.

Whatever method and conditions of transport are chosen for the shipment of the equipment to be repaired under guarantee, in the original packaging, the corresponding costs and the insurance costs will be payable by the customer.

Any damage connected to the return transport of the equipment falls within the framework of the guarantee on the express condition that the customer has sent his complaint within forty-eight hours by registered letter with acknowledgement of receipt to the carrier. A copy of the letter should be sent to SCHOTT INSTRUMENTS.

For equipment with a guaranty card, this is only applicable if the card delivered with the equipment is returned to SCHOTT INSTRUMENTS duly completed.

SOFTWARE GUARANTEE

The software is guaranteed by the designer or the distributor of the software under the conditions specified in the literature accompanying the aforementioned software packages.

Under no circumstances whatsoever will SCHOTT INSTRUMENTS supply any type of guarantee for software packages.

By express agreement, all damages, notably for staff costs, lost of earnings, business trouble, etc are strictly excluded from our guarantee.

The customer is informed that the software cannot be guaranteed exempt from defects or bugs.

3 INSTALLATION

The SCHOTT INSTRUMENTS equipment has been designed, manufactured, tested and inspected according to the ISO 9001 standards.

If the unit is not immediately installed, it should be stored in a dry and clean area. The storage temperature should be between 10 and 35°C.

SCHOTT INSTRUMENTS equipment is carefully inspected before it is packed. As soon as you receive your equipment, check the condition of the packaging and if you notice any problems, notify your carrier within 48 hours. Then consult the packing list and check that everything is in order. Finally, if you discover that something is missing, or if the goods are damaged immediately notify SCHOTT INSTRUMENTS.

IMPORTANT:

In order to benefit from SCHOTT INSTRUMENTS's service (application notes, SCHOTT INSTRUMENTS information, technical assistance, etc.) immediately complete the attached guarantee card and return it to the following address:

SCHOTT INSTRUMENTS

Hattenbergstraße 10

D-55122 Mainz

GERMANY

Phone. : +49 6131 66 5111

Fax : +49 6131 66 5111

E-mail : support@schottinstruments.com

4 THEORETICAL REMINDER

4.1 OPTICAL BEAM

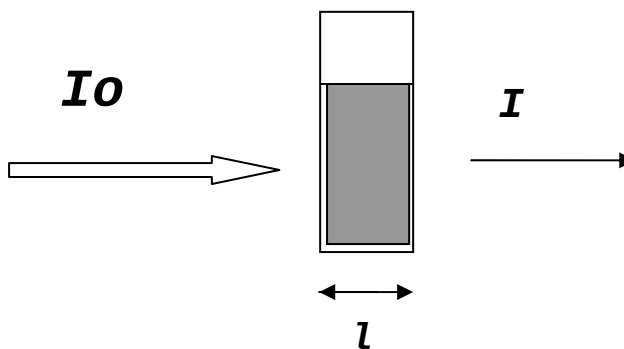
The polychromatic light emitted by a halogen lamp or deuterium lamp, is broken down into monochromatic radiations after reflection on a grating. Once the monochromatic light corresponding to the maximum absorption of the solution to be analyzed has been selected, it crosses the sample where it will be partially absorbed

4.2 BEERT-LAMBERT LAW

Let's consider a beam of monochromatic light with an intensity I_0 which crosses a cell with flat parallel faces containing an absorbing solution.

Upon crossing the solution, the beam with an intensity I_0 is attenuated in accordance with the Beer-Lambert law

$$I = I_0 e^{-\epsilon l C}$$



Where :

$$\log \frac{I_0}{I} = \epsilon l C$$

Where: ϵ is molar absorption coefficient of the substance.
 l is the length of the cell, generally 1 cm.
 C is the concentration of the solution looked for in the cell.

LIMITS OF THE BEER-LAMBERT LAW

- * The light must have a narrow spectrum, preferably a monochromatic one.
- * The wavelength used must correspond to the maximum absorbance of the compound. This requirement allows to work with the highest sensitivity.
- * There must be no ionization, association or solvation of the compound depending on concentration or over time.
- * The solution must not be too concentrated for the law only applies below a certain concentration and for a given substance.

4.3 DÉFINITIONS

4.3.1 Transmittance

The transmittance T (or transmission factor) is expressed as a percentage and is equal to

$$T = \frac{I}{I_0} = e^{-\varepsilon l C}$$

It is generally expressed in %

Transparent body: $T = 100\%$

Opaque body: $T = 0$

4.3.2 Absorbance

Absorbance (A) or extinction (E) is given by the following equation:

$$A = \log \frac{I_0}{I} = \varepsilon l C$$

Transparent body : $A = 0$

Opaque body : $A \rightarrow \infty$

Extinction (E) or absorbance (A) are more frequently expressed as the log of the ratio I_0/I

Absorbance is sometimes called the optical density but such terms are not appropriate. It strictly corresponds to the fraction of the internal optical density of a solution due to a number of its components.
The most common expression is as follows:

$$E = \varepsilon l C$$

4.3.3 Concentration

The concentration of a solution is the quantity of dissolved material per volume unit of solvent.
It is given by the following equation:

$$C = \frac{A}{\varepsilon l}$$

Where: ε is molar absorption coefficient of the substance

l is the length of the cell, generally 1 cm

C is the concentration of the solution looked for in the cell

A is the absorbance of the solution

When the optical path is constant and equal to 1cm, (l is therefore constant), the concentration of the solution will only depend on the absorbance (measured by the instrument) and the molar absorption coefficient (typical physical constant of the substance to be studied for a given wavelength).

TWO ALTERNATIVES:

ε is known, it is given on the data sheet of the reagent used.

Then, the calculation formula used is:

$$C = AF$$

F : Coefficient or factor.

When l is equal to 1 cm:

$$F = \frac{1}{\varepsilon}$$

ε is not known, it can be computed from a standard with a known concentration the absorbance of which will be measured. Then it will directly compute the concentration of the different samples to be analyzed.

$$F = \frac{(C)_{\text{étalon}}}{(A)_{\text{étalon}}}$$

The concentration of the different samples will be calculated directly.

4.3.4 Kinetic

It is the continuous measurement of absorbance in relation to time and curve processing (see details page 103)

4.3.5 Scanning

It is the measurement of absorbance or transmission variation in relation to the wavelength and curve processing (see chapter page 91)

5 CONNECTION AND STARTED

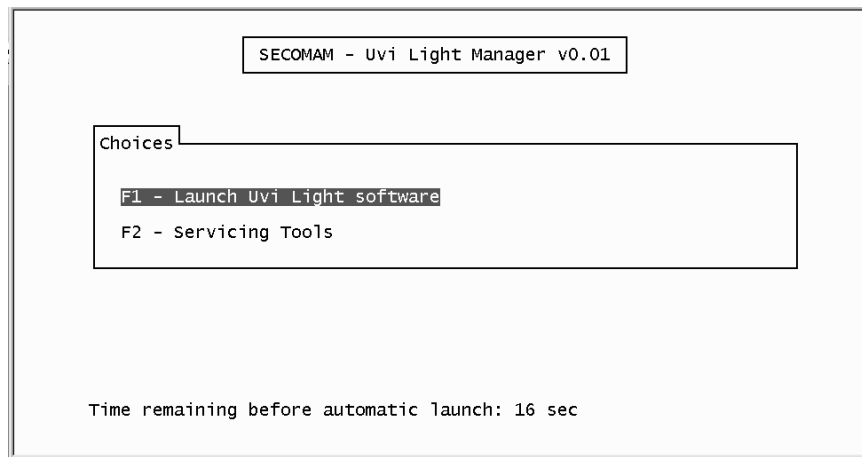
To connect the spectrophotometer see installation guide REF: 0M8039.

Switch on the instrument.

The blue LED (on the unit front) starts flashing.

The user can heard the noise of the filters holder (filters which cut straylight) when it sets its place during the autotest.

35 seconds later, the display is:



2 choices :

- Run the software by pressing **F1 (Launch Uvi Light software)** or let the software run automatically after 20 seconds.
- To have access to the servicing tools by pressing **F2 (Servicing Tools)**.

NOTE: If anomalies are detected (connection cable disconnected, beam completely stopped) to prevent doing autotest correctly, 4 minutes after launching the application, the software will display the following requests:

« **Want you to start again the autotest?** »

If the user answers NO, it displays:

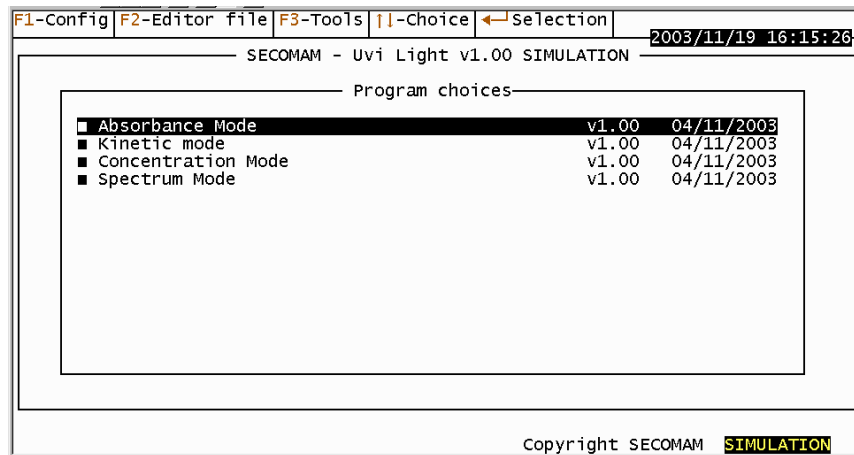
«**Warning: No measure is possible. Pass over the autotest?**»

If the user answers YES, the software will run in **SIMULATION MODE**.

5.1 LAUNCHING OF THE SOFTWARE

- Press **F1 (Launch Uvi Light software)**.

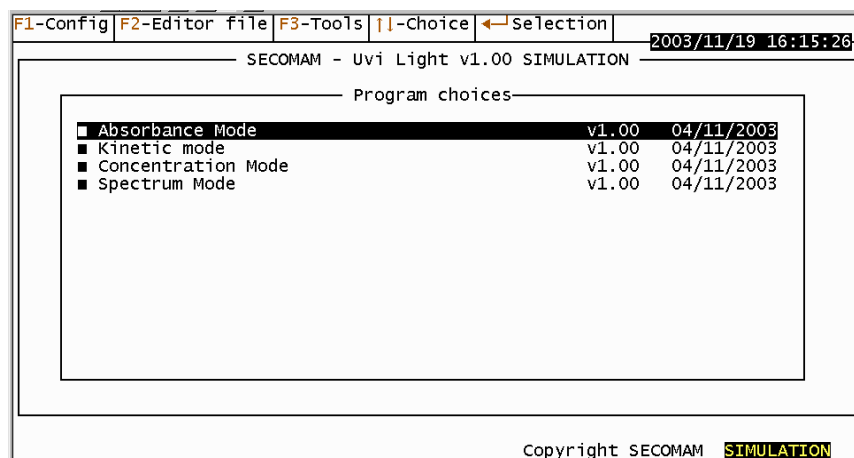
Less than 2 minutes later, the main menu will be displayed:



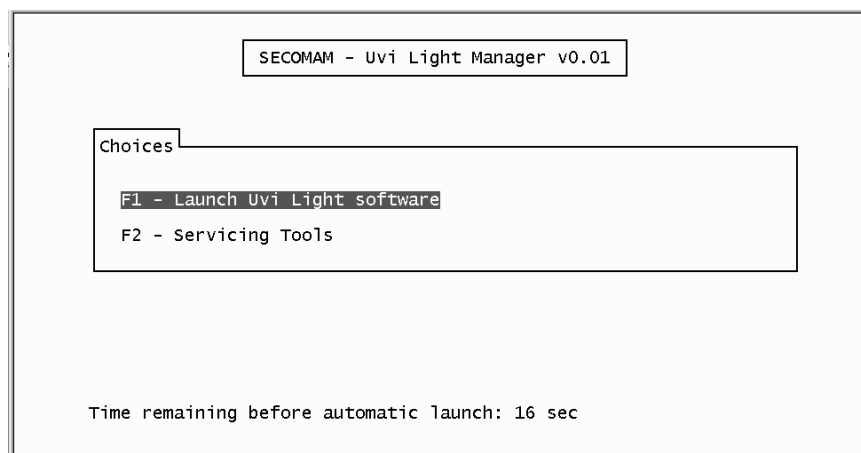
If the printer is connected, the Uvi Light spectrophotometer will print the following autotest report:
The Uvi Light spectrophotometer is ready to work.

5.2 STOP OF UVILIGHT

Come back to the following screen:



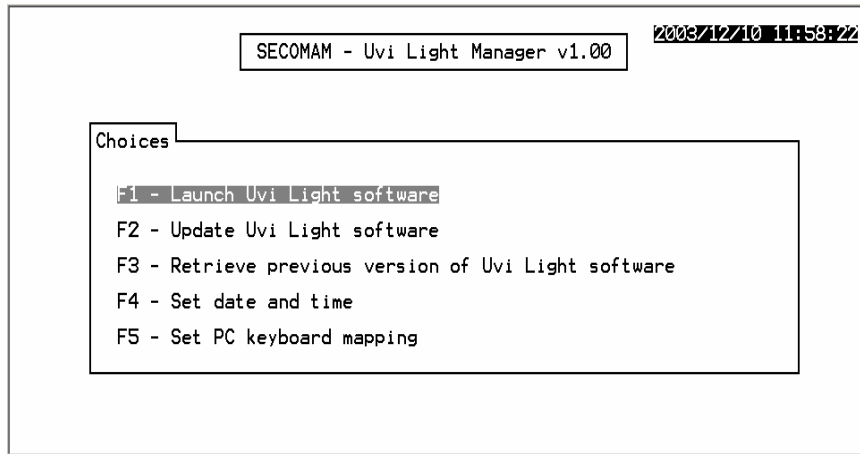
Press « Esc ».



Then, the user can switch off Uvi Light spectrophotometer.

5.3 SERVICING TOOLS

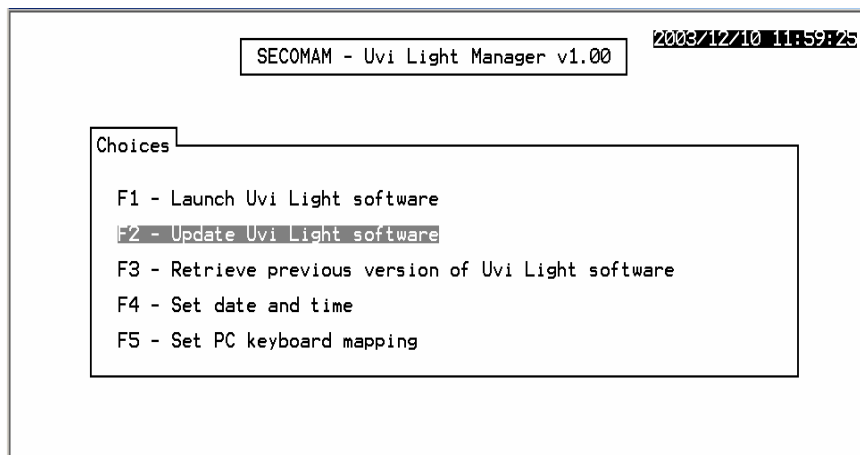
- Press **F2** (Servicing Tools).



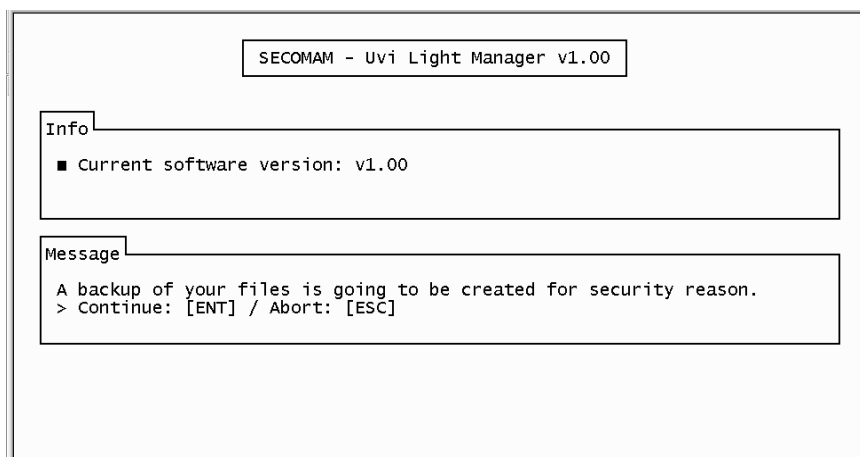
5.3.1 Update Uvi light software

WARNING: this update procedure is available only with diskette supplied directly by SCHOTT INSTRUMENTS

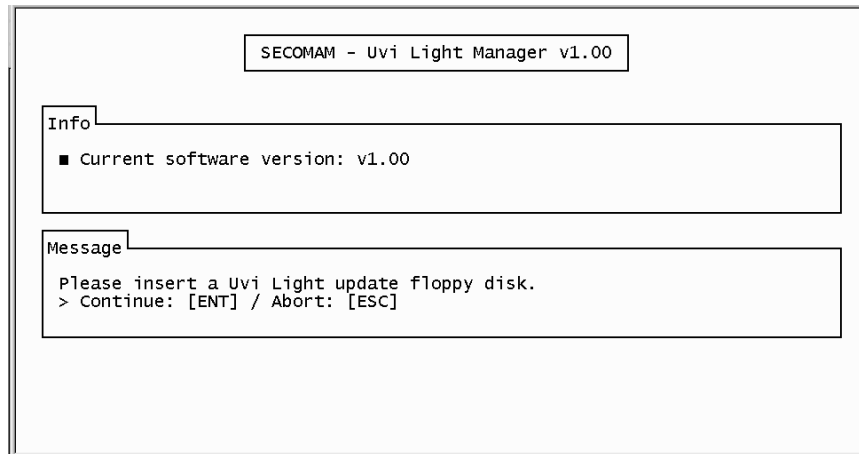
From this screen:



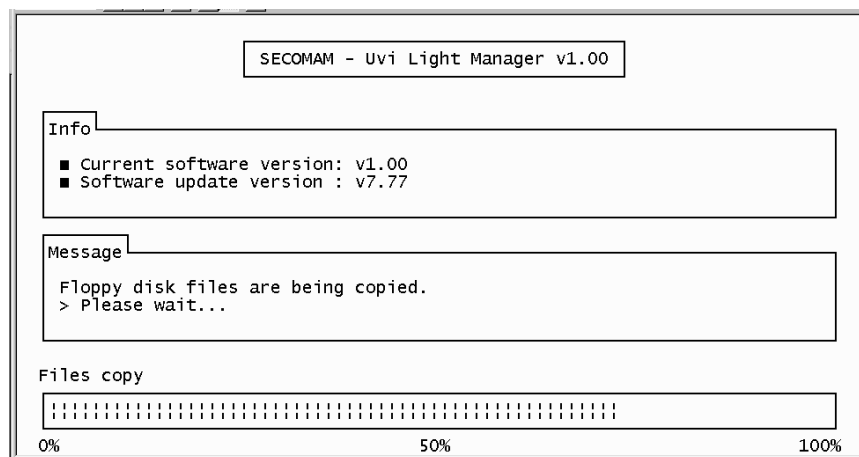
Press **F2** or valid.



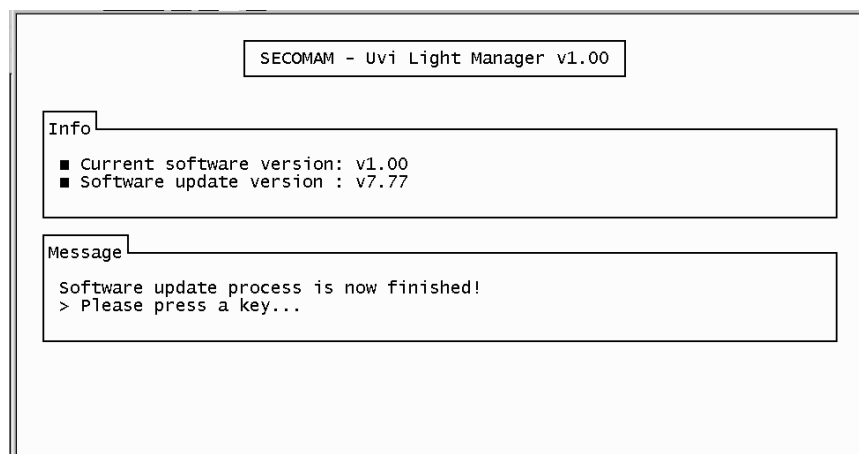
Inside the upper frame, it displays the actual version of the software
Press **Esc (Abort)**. Then the software comes back to the main menu.
Before to import new version of the software, it is important to save the previous version.
Taper **ENT (Continue)**.



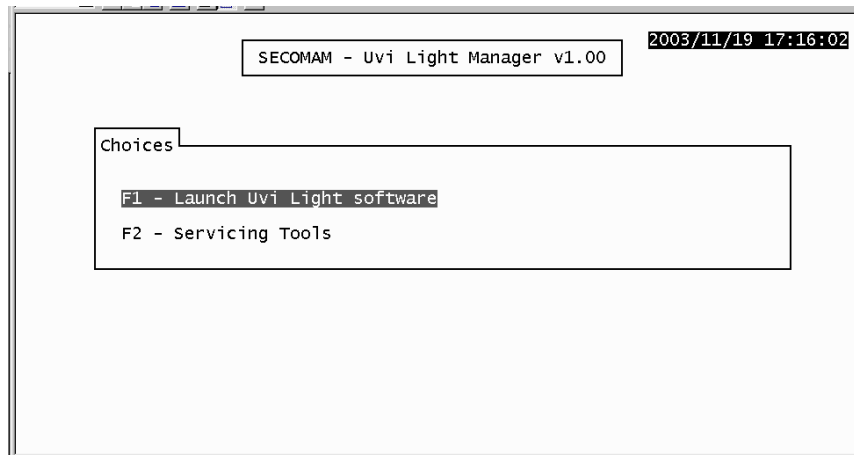
Insert in floppy drive, the new version of the software and press « **ENT** ».



When the files are copied, the display is:



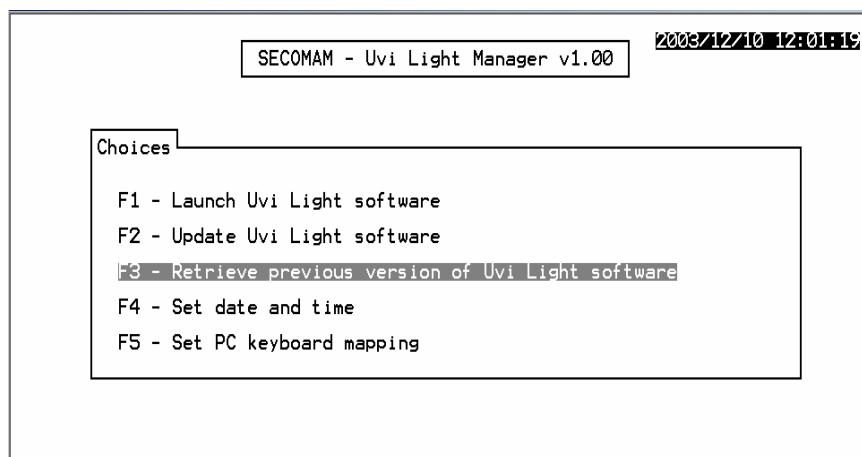
Press any key.



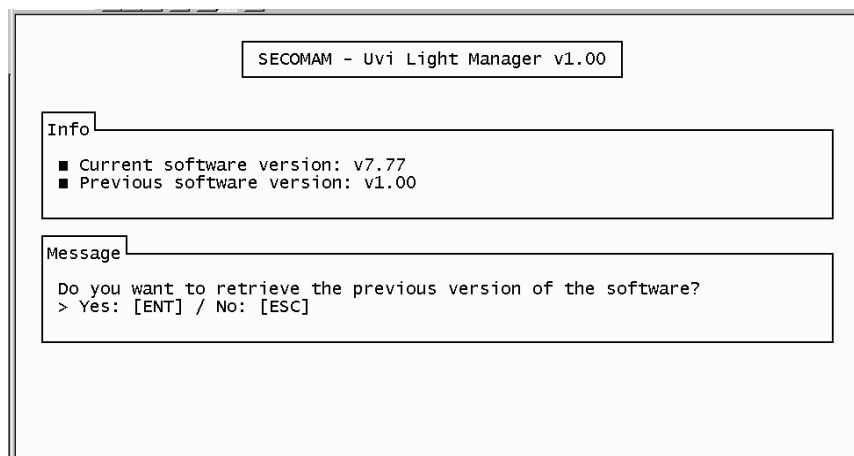
Run the new software version by pressing **F1**.

5.3.2 Retrieve previous version of Uvi light software

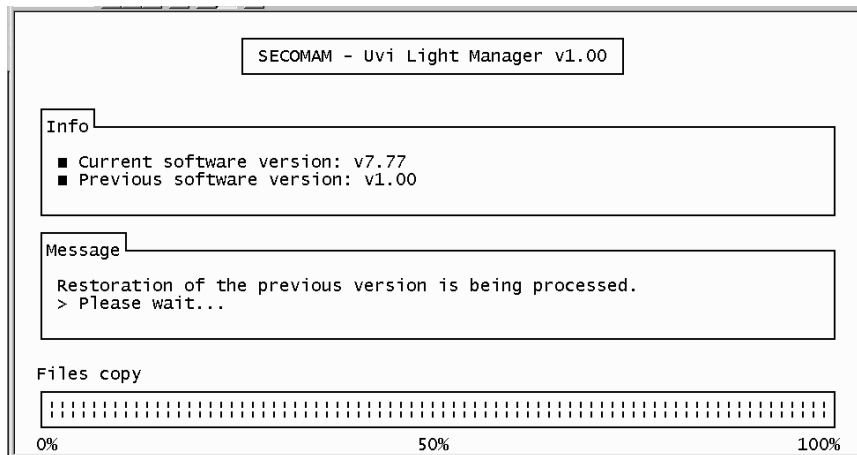
From that screen:



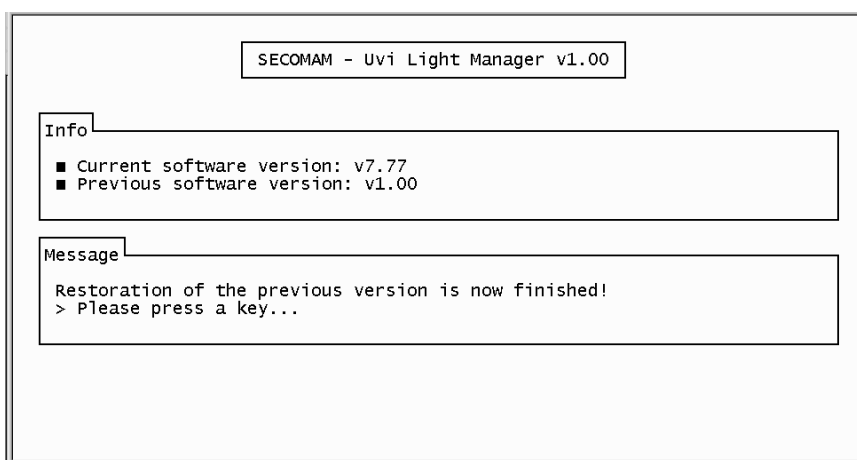
Press **F3** or valid.



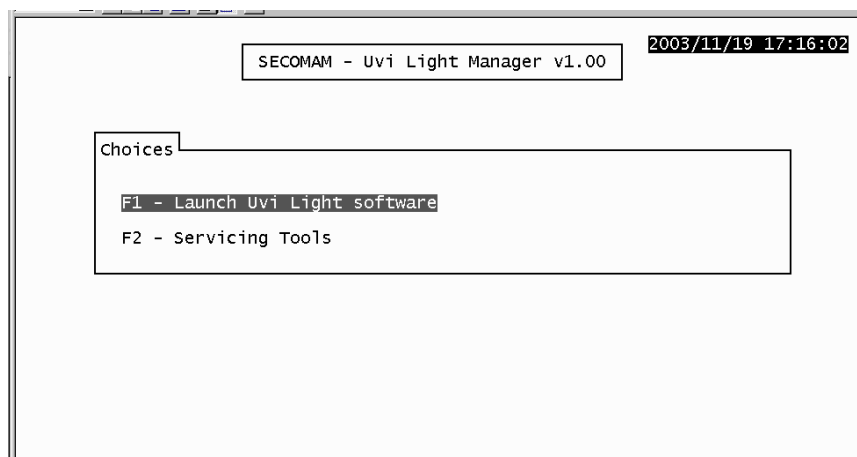
Press « **ENT** ».



When the previous version is restored, the display is:



Press any key.



Run new software version by pressing **F1**.

5.3.3 Error messages

You will find here under different error messages which can appear during software updating.

In these cases:

- verify if the floppy disk contains the new software version.
- verify if the floppy disk is not damaged.
- switch off and on the spectrophotometer and start again the different operations.

Message 1

SECOMAM - Uvi Light Manager v1.00

Info

■ Current software version: v0.00

Message

An error has occurred while backuping the files. Retry?
> Yes: [ENT] / No: [ESC]

Files copy

0%50%100%

Message 2

SECOMAM - Uvi Light Manager v1.00

Info

■ Current software version: v1.00

Message

Floppy disk is not a software update or is defective. Retry?
> Yes: [ENT] / No: [ESC]

Message 3

SECOMAM - Uvi Light Manager v1.00

Info

■ Current software version: v1.00
■ Software update version : v2.35

Message

Error while creating update directory. Retry?
> Yes: [ENT] / No: [ESC]

Message 4

SECOMAM - Uvi Light Manager v1.00

Info
 ■ Current software version: v1.00
 ■ Software update version : v2.35

Message
 Error while copying files from floppy disk. Retry?
 > Yes: [ENT] / No: [ESC]

Files copy

0%
50%
100%

Message 5

SECOMAM - Uvi Light Manager v1.00

Info
 ■ Current software version: v1.00

Message
 There is no floppy disk in drive! Please insert a floppy disk.
 > Continue: [ENT] / Abort: [ESC]

Message 6

SECOMAM - Uvi Light Manager v1.00

Info
 ■ Current software version: v1.00
 ■ Software update version : v2.35

Message
 Error while overwriting software files. Retry?
 > Yes: [ENT] / No: [ESC]

Files copy

0%
50%
100%

5.3.4 Set date and time

From that screen:

SECOMAM - Uvi Light Manager v1.00

2003/12/10 12:02:45

Choices
 F1 - Launch Uvi Light software
 F2 - Update Uvi Light software
 F3 - Retrieve previous version of Uvi Light software
F4 - Set date and time
 F5 - Set PC keyboard mapping

Press **F4** and valid.

SECOMAM - Uvi Light Manager v1.00

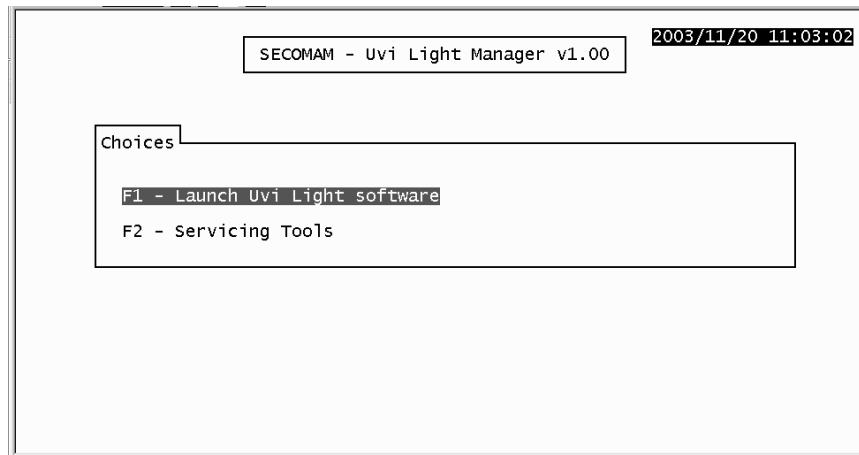
Date and time
 ■ Day (DD): _

Enter data in following order:

SECOMAM - Uvi Light Manager v1.00

Date and time
 ■ Day (DD): 20
 ■ Month (MM): 11
 ■ Year (YYYY): 2003
 ■ Hour (HH): 11
 ■ Minute (MM): 03_

Valid data.



Verify, at the top right side of the screen, inside black frame, if date and hour are updating.
Run software by pressing **F1**.

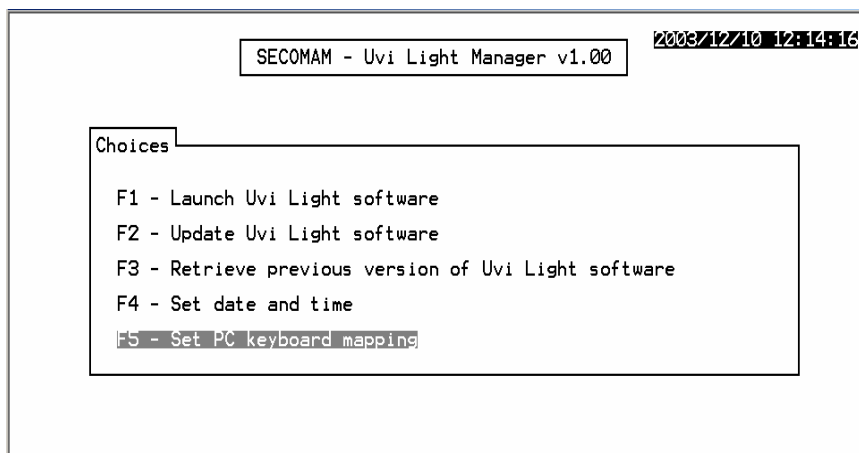
5.3.5 Set external keyboard mapping

Independently of the language used in the software, the operator can adapt the external keyboard to the country where he is.

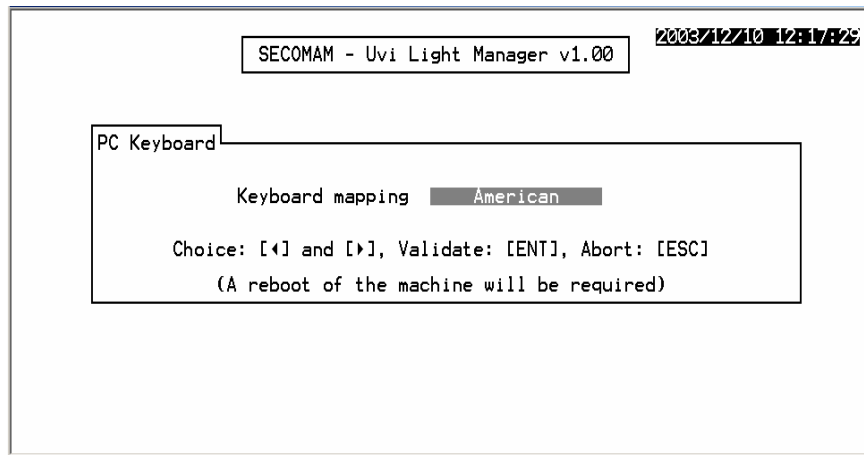
Example

U.S.A.: → « QUERTY » keyboard.
FRANCE → « AZERTY » keyboard.
And so on.

Several choices are proposed:
U.S., English, French, German or Italian keyboard.
From this screen:



Press **F5** or confirm.



Chose the type of keyboard with right and left arrow keys

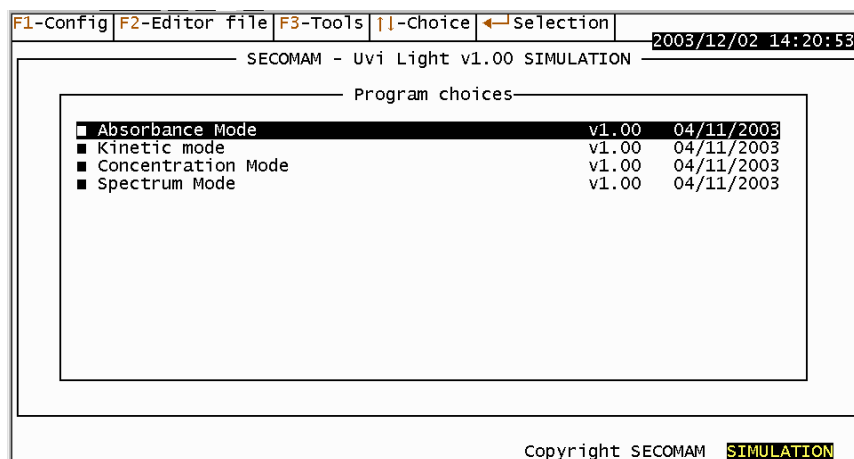
Choisir le type de clavier avec les flèches droite et gauche.

Confirm with [ENT] key.

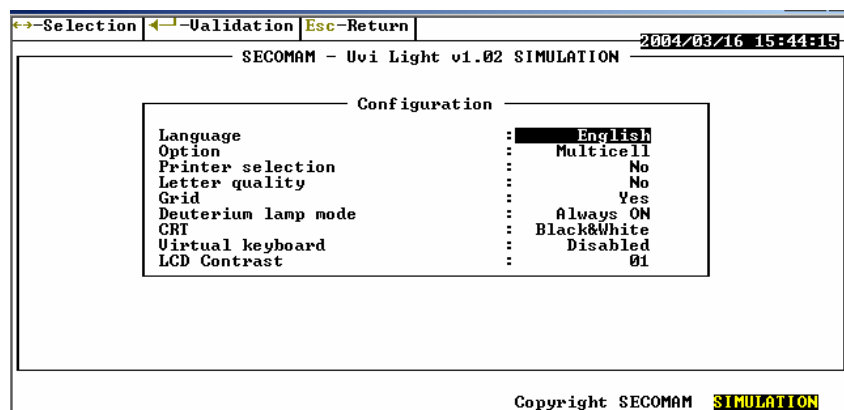
Cancel the configuration with [ESC] key.

6 CONFIGURATION.

The whole Uvi Light can be configured when the main menu is displayed.



Press **F1 (Configuration)**.



See page 29 for changing a parameter.

The various choices for the different parameters are as follows:

1. Language: French, English.
2. Option: No, Pump, Multicell.
3. Printer selection: No, Epson, IBM, HP B/W
4. Letter quality: Yes, No
5. Grid: Yes, No
6. Deuterium lamp: Always On, Stand-By
7. CRT: White & black, Color1, Color2
8. Virtual keyboard: Enable, Disable
9. LCD Contrast: Step from 01 to 63

Explanations of parameters

Line 1

Choice of the working language

Line 2

Choice of accessories used: No accessory connected External peristaltic pump or Multicell holder.

NOTE: If the multicell holder is installed and the corresponding option is not selected (Option: No), the spectrophotometer will detect it and the user will be able to position each cuvette in front of the beam with the keys **SHIFT+F1 to F10**.

F1 = A Position, F9 = I Position, F10 = Zero Position.

WARNING: These commands are available, only if an external alphanumeric keyboard is connected.

Line 3

Choice between the following printer standard (IBM, EPSON or HP PCL) It is also possible to work without printer connected. So select **"No"** for no printer connected.

Line 4

Choice of impression quality

Line 5

Possibility of a gradation grid on the curves

Line 6

Continuous or standby operation of the deuterium lamp (see below).

Line 7

Allow to select three different contrast of the LCD display.

Line 8

When no external keyboard is connected to the spectrophotometer, it is possible to make a virtual alphanumeric keyboard appears at the bottom of the screen to help the user to program.

Line 9

Gradual modification of LCD display contrast.

01 LCD display black

63 LCD display white

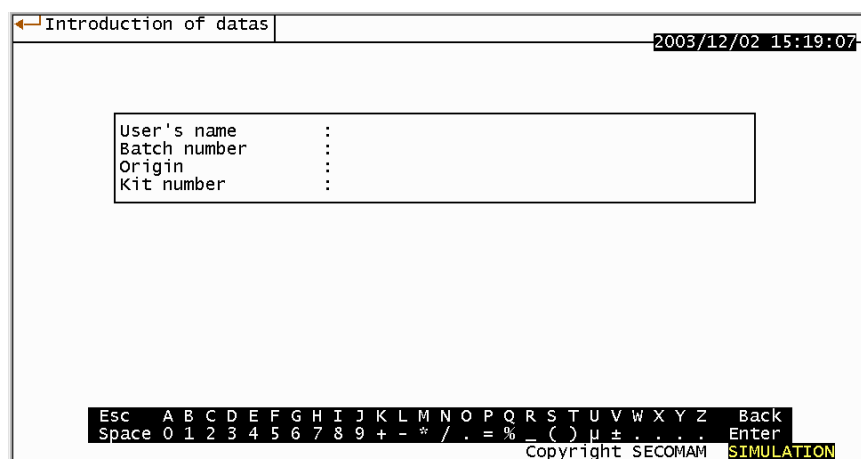
Once all parameters have been entered, confirm.

VIRTUAL KEYBOARD

Once virtual keyboard has been selected, it automatically appears with each time the user must enter alphanumeric characters.

The keyboard takes account of:

- capital alphabet letters only.
- numbers,
- signs (/%=(),.....),
- function keys as Esc, Space, Back, Enter



The choice of the different characters of this keyboard is made with the help of the mouse.

If the external keyboard and the mouse are not connected, the choice is made with the help of ←, →, ↑, ↓ keys and the character validation, including function keys, with **F10 key**.

SWITCHING OFF THE DEUTERIUM LAMP (UV)

When the Standby mode is chosen by the operator, the deuterium lamp switches off after **30 min** only if the user stays in the main menu. If the user enters in a method of analysis before the deuterium lamp turning off, this one will be continually on.

Upon a solicitation (measure between 190 and 330nm) in an analysis mode, for a punctual reading, the deuterium lamp switches on, the message "Waiting for deuterium light" is displayed for 30 secondes and the operator may perform the measure.

The deuterium lamp will turn off again after **30 min** upon returning to the main menu.

7 PRINCIPLE FOR MENUS AND COMMAND OF UVI LIGHT

The overall structure of the program is of the tree type, each branch having ramifications and so forth.

To move through the structure, the program proposes at each step a menu on the top line of the screen with all the possibilities offered to the operator. For example, after reading a sample in "Spectrum Mode", the menu is as follows:

F1 (Measure) F2 (Parameters) F3 (Tools) Esc (Quit)

To have access to any of the sub-routines, press the key corresponding to the option selected:

Example: Press **F3 (Tools)**. The following menu is displayed:

F1 (I/O) F2 (Scales) F3 (Calculation) F4 (Note) F5 (Windows) F6 (Abs.) F7(Trans.) Esc (Quit)

Press **F3 (Calculation)**, the following menu is displayed:

F1 (Abs.) F2 (Derivative) F3 (Maxi) +/- (Operation) F6 (Constant) F7 (Ratio) Esc (Quit)

As a rule, presentation on the monitor will be as follows:

A first line with the choice such as: **F1 (Measure)**, **F1 (I/O)** or **F2 (Derivative)**,...

A second line with instructions such as : "**Ready for measure of zero?**" or "**Authorized measure**"...

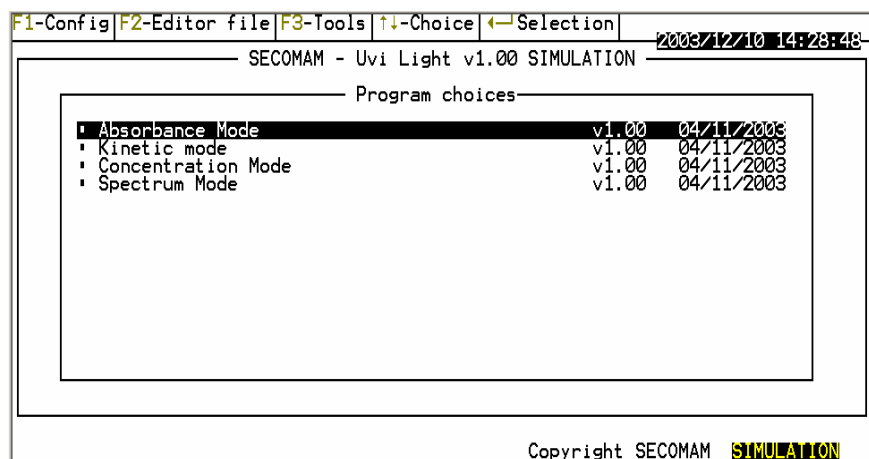
A large frame with on the right the parameters of the analysis in process and on the left the results or a curve.

The last line with operations in process such as "**Storage of the baseline**" or "**Saving in process**" ...

8 ANALYSIS MODES

8.1 RESIDENT MODES

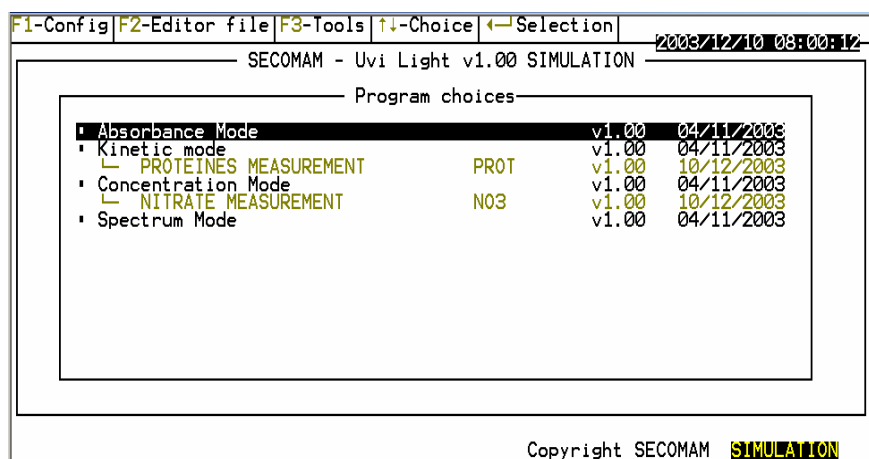
They are the measuring modes included in the software



Absorbance: continuous measurement of absorbance and transmittance
Kinetics: follow-up measurement of absorbance in relation with time and curve processing.
Concentration: general programs for quantitative readings [concentration, multiple calibrations (linear or not), calibrated kinetics, multiple wavelength]
Spectra: spectral scanning and curve processing.

These measuring mode are displayed with their version number and creation date.

8.2 CUSTOMIZED METHODS (USER'S)



These are those that the operator has saved under a given name (ex: PROTEINES MEASUREMENT, NITRATE MEASUREMENT) to use the same parameters again.

In the tree structure of main menu, every method is saved by the operator as a routine of the mother method used to create it.

Example:

"PROTEINES MEASUREMENT" was created from kinetic mode.

"NITRATE MEASUREMENT" was created from concentration mode.

Short names (PROT, NO3,...) which appear on the right side of saved methods are the names of the files containing the methods parameters.

8.2.1 Applications created

These are original applications created by the operator or SCHOTT INSTRUMENTS from the **SPECTRO PASCAL** software. As a rule, they can give rise to several types of readings (spectra, absorbance reading for a given wavelength, control for an accessory not supplied by SCHOTT INSTRUMENTS).

The software is made from the editor program.

9 ALTERING THE PARAMETERS

The procedure for altering the parameters is very simple. It is the same whatever the position of the operator in the program and whatever the analysis mode or method used.

Select a measuring mode. Ex: KINETIC.

Confirm.

With the mouse or virtual keyboard, enter:

- User's name (20 characters: signs, letters and numbers).
- Batch number (8 characters: signs, letters and numbers).
- Samples origin (30 characters: signs, letters and numbers).
- Reagent kit number (8 characters: signs, letters and numbers).

This information is useful for measurements traceability (G.L.P., ISO 9000,...) and will be printed with the results

F1-Execute F2-Parameters F3-File results Esc-Quit		2003/12/10 08:30:52	
Kinetic mode v1.00			
PARAMETERS		RESULTS	
Wavelength (nm):	540		
Lag time (0-1800s):	60		
No of segments (1-100):	4		
Segment time(30-13000):	30		
Calculation :	Regre		
Decimal place (0-3):	0		
Factor (+/-10000):	1000		
Unit (Speed):	G/L		
Substrate unit (Micha):	μMOL/L		
Numbering :	Auto		
Parameters locked :	No		
Copyright SECOMAM SIMULATION			

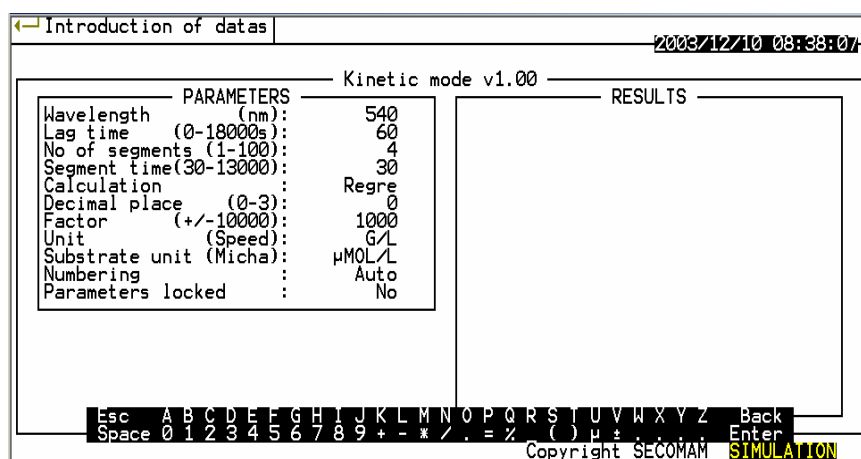
The parameters of the analyses can be found in a window on the left-hand side of the screen.

For programming new parameters, enter **F2 (Parameters)**.

F1-Modification F2-Printer F3-Save Esc-Return		2003/12/10 08:34:36	
Kinetic mode v1.00			
PARAMETERS		RESULTS	
Wavelength (nm):	540		
Lag time (0-1800s):	60		
No of segments (1-100):	4		
Segment time(30-13000):	30		
Calculation :	Regre		
Decimal place (0-3):	0		
Factor (+/-10000):	1000		
Unit (Speed):	G/L		
Substrate unit (Micha):	μMOL/L		
Numbering :	Auto		
Parameters locked :	No		
Copyright SECOMAM SIMULATION			

Print the parameters by entering **F2 (Printer)**. For changing one or several parameters, enter **F1 (Modification)**. Press **F3 (Save)** to save parameters.

Press **F1 (Modification)**.



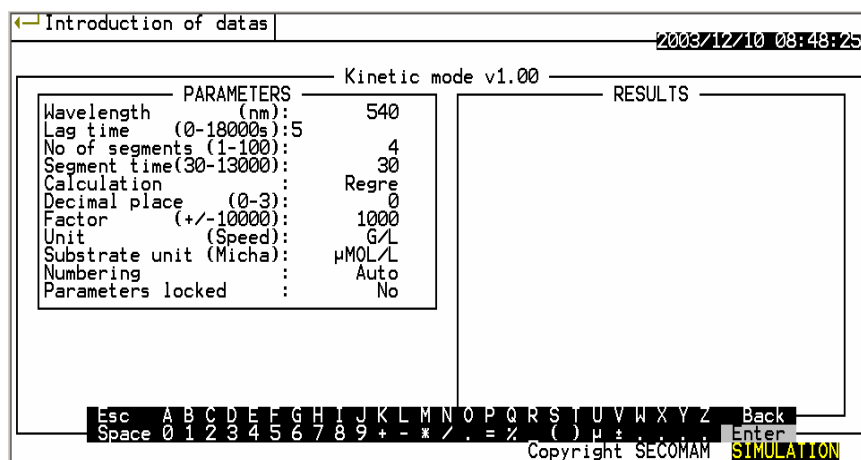
9.1 SELECTION OF A PARAMETER

A cursor blinks on the first line. Just move the cursor within the window by means of keys $\uparrow$ and $\downarrow$ and place it in front of the parameter to be modified. If there are too many parameters for the window, they will be displayed by keeping the $\downarrow$ key down when the cursor is at the bottom of the window.

9.2 MODIFICATION OF A PARAMETER

There are two alternatives.

9.2.1 The parameters is entering by the operator



By means of keys $\uparrow$ and $\downarrow$ place the cursor in front of the parameter to be modified. Use external keyboard or virtual keyboard with mouse to enter new value. Confirm.

"Backspace" key allows to delete an error.

NOTE: If the operator does not valid the new value with “Enter” key and goes to the next parameter with ↓ key, the parameter will take back its previous value.

9.2.2 The nature of the parameter is preset

The parameter is chosen among several parameters or values proposed by the Uvi Light.

←→-Selection		←-Validation	Esc-Escape	2003/12/10 09:01:34	
Kinetic mode v1.00					
PARAMETERS			RESULTS		
Wavelength (nm):	540				
Lag time (0-18000s):	5				
No of segments (1-100):	4				
Segment time(30-13000):	30				
Calculation :	Regre				
Decimal place (0-3):	0				
Factor (+/-10000):	1000				
Unit (Speed):	G/L				
Substrate unit (Micha):	μMOL/L				
Numbering :	Unit				
Parameters locked :	No				
Copyright SECOMAM SIMULATION					

In such case, choose the parameter or the value by means of the ← and → keys. Scroll the parameters. Once the selection is completed, confirm.

9.3 VALIDATION OF ALL THE PARAMETERS

It is very important to confirm every parameter line in order to confirm all parameters. If the operator press "ESC" key before to reach last parameter line, all parameters modifications will be cancelled.

9.4 SPECIFIC CASE: PARAMETERS FOR A CONCENTRATION READING

Select the CONCENTRATION analysis mode.

Press **F2 (Parameters)**, then **F1 (Modification)**.

←→-Selection		←-Validation	Esc-Escape	2003/12/10 09:12:50	
Concentration Mode v1.00					
PARAMETERS					
Type of measure :	Abs				
Wavelength (nm):	500				
Reagent blank :	No				
Sample blank :	No				
Decimal place (0-3):	1				
No of standards (0-10):	1				
Concentration(0-10000):	10.0				
Unit :	g/l				
Numbering :	Auto				
Parameters locked :	No				
Copyright SECOMAM SIMULATION					

The screen displays two windows on the left-hand side.

The first one allows to select the analysis mode (measurement of absorbance with reference to a coefficient, a standard or a calibration range, 2-point kinetic reading, multiple wavelength reading).

The second one is the window linked to the analysis modes.

In the first window, to change the parameter, select the measuring mode with ← and → keys. Then confirm.

Ex:

←-Selection	←-Validation	Esc-Escape	2003/12/10 10:06:02																																							
Concentration Mode v1.00																																										
PARAMETERS Type of measure : MultiWL <table> <tr><td>Reagent blank</td><td>:</td><td>No</td></tr> <tr><td>Decimal place (0-3):</td><td>:</td><td>1</td></tr> <tr><td>No of standards (0-10):</td><td>:</td><td>1</td></tr> <tr><td>Concentration(0-10000):</td><td>:</td><td>10.0</td></tr> <tr><td>Unit</td><td>:</td><td>g/l</td></tr> <tr><td>No of W.L. (2-10):</td><td>:</td><td>2</td></tr> <tr><td>Wavelength 1 (nm)</td><td>:</td><td>190</td></tr> <tr><td>Wavelength 2 (nm)</td><td>:</td><td>190</td></tr> <tr><td>Coeff. comma (0-3):</td><td>:</td><td>1</td></tr> <tr><td>A0 (+/-10000)</td><td>:</td><td>1.0</td></tr> <tr><td>A1 (+/-10000)</td><td>:</td><td>0.0</td></tr> <tr><td>A2 (+/-10000)</td><td>:</td><td>0.0</td></tr> <tr><td>B0 (+/-10000)</td><td>:</td><td>1.0</td></tr> </table> GENERAL CALCULATION $R = \frac{A0+A1*Abs1+A2*Abs2+...+An*Absn}{B0+B1*Abs1+B2*Abs2+...+Bn*Absn}$				Reagent blank	:	No	Decimal place (0-3):	:	1	No of standards (0-10):	:	1	Concentration(0-10000):	:	10.0	Unit	:	g/l	No of W.L. (2-10):	:	2	Wavelength 1 (nm)	:	190	Wavelength 2 (nm)	:	190	Coeff. comma (0-3):	:	1	A0 (+/-10000)	:	1.0	A1 (+/-10000)	:	0.0	A2 (+/-10000)	:	0.0	B0 (+/-10000)	:	1.0
Reagent blank	:	No																																								
Decimal place (0-3):	:	1																																								
No of standards (0-10):	:	1																																								
Concentration(0-10000):	:	10.0																																								
Unit	:	g/l																																								
No of W.L. (2-10):	:	2																																								
Wavelength 1 (nm)	:	190																																								
Wavelength 2 (nm)	:	190																																								
Coeff. comma (0-3):	:	1																																								
A0 (+/-10000)	:	1.0																																								
A1 (+/-10000)	:	0.0																																								
A2 (+/-10000)	:	0.0																																								
B0 (+/-10000)	:	1.0																																								
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Modify the parameters as stated above.

NOTE: In the MultiWL mode, the general calculation formula appears in a window on the right-hand side.

9.5 PRINTING THE PARAMETERS

For printing the parameters when the method of analysis has been loaded, press **F2 (Parameters)**, then **F2 (Printer)**.

The parameters are printed as follows:

```

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi
Light v1.00
Date: Friday november the 21,2003 Time: 11:43 am
User's name: SMITH
Batch number: 123
Origin: HOSPITAL
Kit number: 1256

Method : Kinetic Mode v1.00

Parameters:

Wavelength (nm)      : 540
Lag time (0-18000s)  : 60
No of segments (1-100) : 4
Segment time (30-13000s) : 30
Calculation          : Regre
Decimal place (0-3)   : 0
Factor (+/-10000)     : 1000
Unit (Speed)         : G/L
Substrate unit (Micka) : µMOL/L
Numbering            : Auto
Parameters locked     : No
    
```

9.6 SAVING THE PARAMETERS

For saving parameters, proceed as follows:

Press **F2 (Parameters)**, **F3 (Save)**.

Give a name (8 characters) to the method. Confirm.

Give a title (30 characters) to the method. Confirm.

10 HOW TO USE WITH SINGLE CELL HOLDER

PLEASE REMEMBER :

To use Uvi Light with single-cell holder is simpler than with multiple-cell holder, that is why the description of measuring mode, in this manual, is given using multiple-cell holder.

However, the arborescence of the software is the same in both cases. The difference lies in the sequence of measure solution (blank, standard, samples, ...)

When using multi-cell holder, user placed the solutions in the cell-holder according to the instructions given by the software. The solutions will be measured in one series per group of 8.

When using single-cell holder, user placed the solutions in the cell-holder one after another successively with respect to the measuring order.

This chapter describes how to measure various solutions using single-cell holder when you want to establish a calibration curve in Concentration mode.

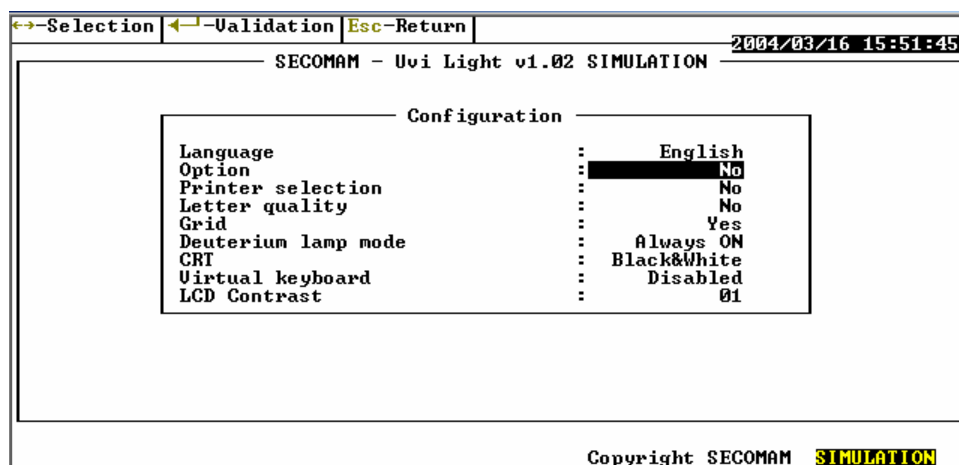
This procedure will be the same for other measuring modes: Absorbance, Kinetics, Spectrum scan.
For more information on these measuring modes, see related chapters for multi-cell holder.

To install the cell-holder, see installation guide.

SELECTING SINGLE-CELL HOLDER

Proceed this way :

- Install the accessory.
- From main menu, press **F1 (F1-Configuration)**.



Modify the parameter "OPTION".

Select "No".

Confirm other parameters in the window.

10.1 MEASURING

From main menu, select a measuring mode (example: Concentration Mode)
Program analysis parameter. Press **F2 (Parameters)** and **F1 (Modification)**.

F1-Modification	F2-Printer	F3-Save	Esc-Quit	2003/12/02 12:04:57
-----------------	------------	---------	----------	---------------------

Concentration Mode v1.00

PARAMETERS	
Type of measure	: Abs
Wavelength (nm):	500
Reagent blank :	Yes
Sample blank :	No
Decimal place (0-3):	1
No of standards (0-10):	4
Conc. 1 (0-10000):	10.0
Conc. 2 (0-10000):	20.0
Conc. 3 (0-10000):	30.0
Conc. 4 (0-10000):	40.0
Unit :	G/L
X axis (Concentration):	Lin
Y axis (Absorbance):	Lin
Type of curve :	Regre

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- Print analysis parameters with **F2 (Print)**.
- Save analysis parameters with **F3 (Save)**.
- Press **Esc (Quit)** to continue.

F1-Execute	F2-Parameters	F3-File results	Esc-Quit	2003/12/02 12:06:26
------------	---------------	-----------------	----------	---------------------

Concentration Mode v1.00

PARAMETERS	
Type of measure	: Abs
Wavelength (nm):	500
Reagent blank :	Yes
Sample blank :	No
Decimal place (0-3):	1
No of standards (0-10):	4
Conc. 1 (0-10000):	10.0
Conc. 2 (0-10000):	20.0
Conc. 3 (0-10000):	30.0
Conc. 4 (0-10000):	40.0
Unit :	G/L
X axis (Concentration):	Lin
Y axis (Absorbance):	Lin
Type of curve :	Regre

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- Create a file to save analysis result with **F3 (File results)**.
- Press **F1(Execute)**.

F1-Measure	F2-Simulation	F3-Parameters	Esc-Quit	2004/03/16 16:23:31
------------	---------------	---------------	----------	---------------------

Measure of Zero

Concentration Mode v1.01

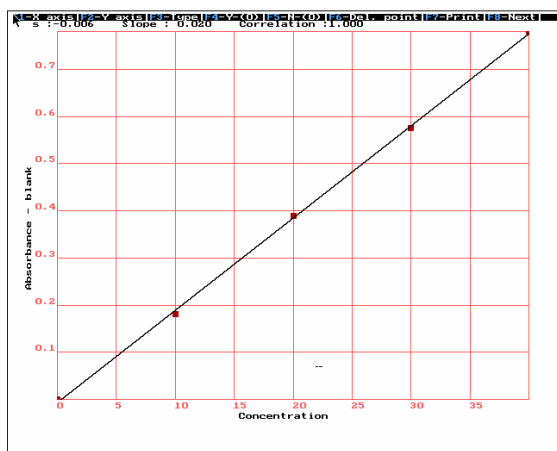
PARAMETERS		RESULTS	
Type of measure	: Abs	Sample	Conc. Abs.
Wavelength (nm):	500		
Reagent blank :	Yes		
Sample blank :	No		
Decimal place (0-3):	1		
No of standards (0-10):	4		
Conc. 1 (0-10000):	10.0		
Conc. 2 (0-10000):	20.0		
Conc. 3 (0-10000):	30.0		
Conc. 4 (0-10000):	40.0		
Unit :	G/L		
X axis (Concentration):	Lin		
Y axis (Absorbance):	Lin		
Type of curve :	Regre		

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- Insert the Zero (Reference) cuvette in place. Press **F1 (Measure)**. After measuring remove the Reference cuvette.
- Insert the Blank cuvette in place. Press **F1 (Measure)**. After measuring remove the Blank cuvette.

F1-Measure		F2-Simulation		F3-Parameters		Esc-Quit		2004/03/16 16:31:12	
Measure of Std. 1									
Concentration Mode v1.01									
PARAMETERS					RESULTS				
Type of measure : Abs					Sample Conc. Abs.				
Wavelength (nm): 500					Blank 0.020				
Reagent blank : Yes									
Sample blank : No									
Decimal place (0-3): 1									
No of standards (0-10): 4									
Conc. 1 (0-10000): 10.0									
Conc. 2 (0-10000): 20.0									
Conc. 3 (0-10000): 30.0									
Conc. 4 (0-10000): 40.0									
Unit : G/L									
X axis (Concentration): Lin									
Y axis (Absorbance): Lin									
Type of curve : Regre									
Copyright SECOMAM SIMULATION									

- Insert the Standard 1 cuvette in place. Press **F1 (Measure)**. After measuring remove the Standard 1 cuvette and then
- Insert the Standard 2 cuvette in place. Press **F1 (Measure)**. After measuring remove the Standard 2 cuvette and then
- Continue this way till the last of the Standard was read.



- Modify the axis with **F1 (X axis)** and **F2 (Y axis)**.
- Modify the type of curve calculation with **F3 (Type)**.
- Delete the points with **F6 (Del. Point)**.
- Print the curve with **F7 (Print.)**.
- Press **F8 (Next)** to go to measuring the samples.

F1-Measure		F2-Simulation		F3-Curve		F4-Parameters		Esc-Quit		2004/03/16 16:34:35	
Measure of Sam. 1											
Concentration Mode v1.01											
PARAMETERS						RESULTS					
Type of measure : Abs						Sample Conc. Abs.					
Wavelength (nm): 500						Blank 0.020					
Reagent blank : Yes						Std. 1 10.0 G/L 0.180					
Sample blank : No						Std. 2 20.0 G/L 0.390					
Decimal place (0-3): 1						Std. 3 30.0 G/L 0.575					
No of standards (0-10): 4						Std. 4 40.0 G/L 0.780					
Conc. 1 (0-10000): 10.0											
Conc. 2 (0-10000): 20.0											
Conc. 3 (0-10000): 30.0											
Conc. 4 (0-10000): 40.0											
Unit : G/L											
X axis (Concentration): Lin											
Y axis (Absorbance): Lin											
Type of curve : Regre											
Copyright SECOMAM SIMULATION											

- Insert Sample 1 in place. Press **F1 (Measure)**.

F1-Measure		F2-Simulation		F3-Curve		F4-Parameters		Esc-Quit		2004/03/16 16:37:37	
Measure of Sam. 2											
Concentration Mode v1.01											
PARAMETERS						RESULTS					
Type of measure : Abs						Sample Conc. Abs.					
Wavelength (nm): 500						Blank					
Reagent blank : Yes						Std. 1 10.0 G/L 0.020					
Sample blank : No						Std. 2 20.0 G/L 0.180					
Decimal place (0-3): 1						Std. 3 30.0 G/L 0.390					
No of standards (0-10): 4						Std. 4 40.0 G/L 0.575					
Conc. 1 (0-10000): 10.0						Std. 1 75.1 G/L 1.462					
Conc. 2 (0-10000): 20.0											
Conc. 3 (0-10000): 30.0											
Conc. 4 (0-10000): 40.0											
Unit : G/L											
X axis (Concentration): Lin											
Y axis (Absorbance): Lin											
Type of curve : Regre											
Copyright SECOMAM SIMULATION											

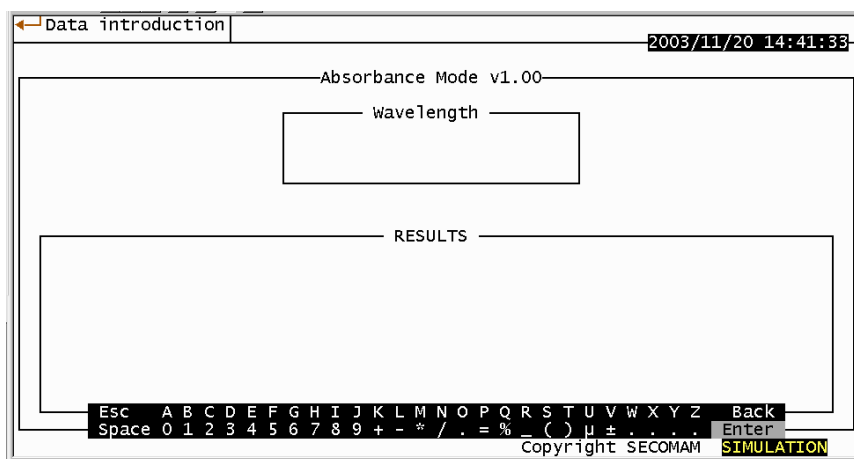
- Insert sample 2 in place. Press **F1 (Measure)** etc.

Automatic print-out of the values of the Standards and Samples.

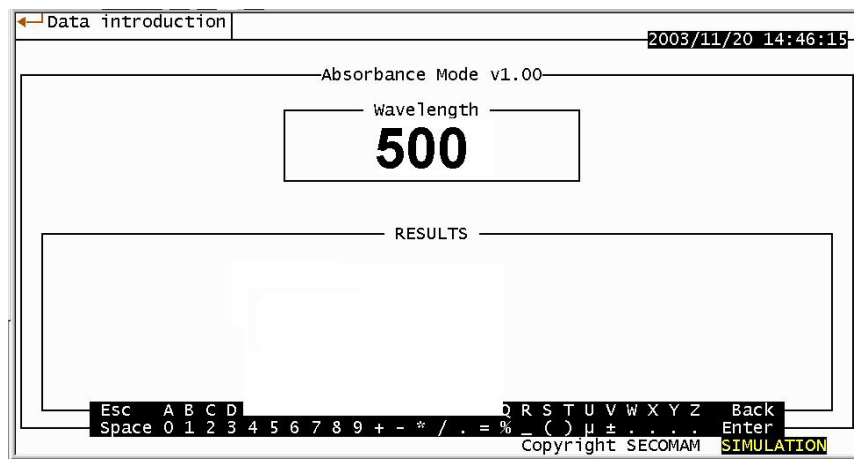
11 ABSORBANCE MODE

This mode allows performing a continuous absorbance and transmittance reading. Select **Absorbance mode** with the $\uparrow\downarrow$ keys. Confirm.

11.1 WAVELENGTH CHOICE

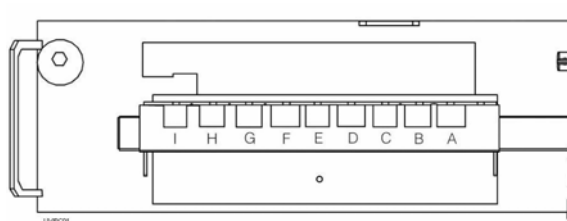


Enter the wavelength and confirm.



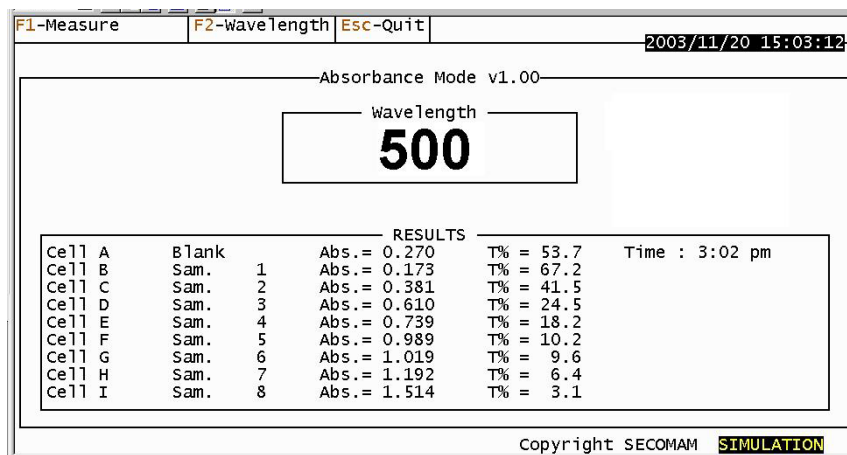
11.2 MEASURE

Prepare multicell holder as follow:



A position: Always blanc (Reagent) or reference solution.
From B to I: Samples.

To start measurement, press **F1 (Measure)**.



At any time, the user can change the wavelength by pressing F2 (Wavelength).

THE DISPLAYED BLANC ABSORBANCE IS READ AGAINST THE AIR.
THE DISPLAYED SAMPLES ABSORBANCES ARE READ AGAINST THE BLANC

The results are printed as follow:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00					
Date : Thursday november the 20,2003 Time : 3 :02 pm					
Absorbance at 500 nm date : Thursday november the 20,2003					
Blank	W.L.= 500 nm	Abs.= 0.299	T% = 50.3	Time : 3:02 pm	
Sam. 1	W.L.= 500 nm	Abs.= 0.185	T% = 65.3		
Sam. 2	W.L.= 500 nm	Abs.= 0.320	T% = 47.9		
Sam. 3	W.L.= 500 nm	Abs.= 0.575	T% = 26.6		
Sam. 4	W.L.= 500 nm	Abs.= 0.751	T% = 17.7		
Sam. 5	W.L.= 500 nm	Abs.= 0.814	T% = 15.4		
Sam. 6	W.L.= 500 nm	Abs.= 1.102	T% = 7.9		
Sam. 7	W.L.= 500 nm	Abs.= 1.348	T% = 4.5		
Sam. 8	W.L.= 500 nm	Abs.= 1.476	T% = 3.3		

"Esc" key allows to exit out of absorbance mode and come back to the main menu.

12 CONCENTRATION MODE

This function allows to use any methods against one or several standards (if necessary without standard if a calibration coefficient is entered) to obtain concentration results or results processed by a mathematical formula.

The readings are: concentration, calibrated kinetics, multiple wavelength.

The concentration programs without standard, with standard and with several standards will be studied in detail.

N.B.: the principle of the other two measuring methods, i.e. calibrated kinetics and multiple wavelength will be defined. As regards use with a coefficient, a standard or several standards, frequent references will be made to the description of the concentration mode.

Furthermore either of the three modes will be selected by changing one of the parameters in the table: Type of measure.

12.1 CONCENTRATION MEASUREMENT

From the main menu, select “**Concentration mode**”. Confirm.

Introduction of datas 2003/11/20 16:10:40

User's name	:	SMITH
Batch number	:	123
Origin	:	HOSPITAL
Kit number	:	1256

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % _ () µ ± Enter
Copyright SECOMAM SIMULATION

With the help of mouse or virtual keyboard enter:

- User's name (20 characters: signs, letters and numbers).
- Batch number (8 characters: signs, letters and numbers).
- Samples origin (30 characters: signs, letters and numbers).
- Reagent kit number (8 characters: signs, letters and numbers).

This information is useful for measurements traceability (G.L.P., ISO 9000,...) and will be printed with the results

- Press **Esc** if the user wants to pass this stage.

12.1.1 Programmation of parameters

See page 29

From main menu, Press **F2 (Parameters)** and **F1 (Modification)**.

Introduction of datas 2003/11/21 09:05:17

Concentration Mode v1.00

PARAMETERS

Type of measure : Abs

Wavelength (nm): 500

Reagent blank : No

Sample blank : No

Decimal place (0-3): 1

No of standards (0-10): 2

Conc. 1 (0-10000): 10.0

Conc. 2 (0-10000): 20.0

Unit : g/l

X axis (Concentration): Lin

Y axis (Absorbance): Lin

Type of curve : Linear

Numbering : Auto

Parameters locked : No

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back

Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % _ () µ ± Enter

Copyright SECOMAM SIMULATION

* Type of measure

Abs-2pt kin-Multi WL

Calibrated quantitative methods.

Choose Abs.

* Wavelength

190 - 900nm.

* Reagent blank

YES – NO. See blanks meaning at the end of this chapter page .80

* Sample blank

YES – NO. See blanks meaning at the end of this chapter page .80

* Decimal place

From 0 to 3

Precision of the result.

* Standard number

Factor

To work with factor, answer 0.

Choose value between +/- 10000.

1 Standard

To work with 1 standard, answer 1.

Choose value between 0 and 10000.

Several standards

To work with factor, enter the number of standards (from 2 to 10).

Choose value between 0 and 10000.

* Unit

With keyboard , enter the abbreviation of unit.

* X axis (concentration axis)

Linear or logarithmic.

* Y axis (absorbance axis)

Linear, logarithmic, 1/Abs (1/Y) or Logit. . See Logit axis meaning at the end of this chapter page 80

* Type of curve

Linear (segmented curve), "Regre" (linear regression), "Regre (0)" (linear regression going through the origin 0), Spline. See explanation on the type of curve at the end of this chapter page 81

* Numbering

This parameter concerns samples identification.

Auto: Identification of the sample is numerical and increasing.

Example: Sam.1, Sam.2,...

Unit: The user assigns a name to each sample (8 characters) and eventually attributes a dilution factor. See explanation at the end of this chapter, page 88.

Table: The user prepares a table in which he will enter the number of samples, their name, and the dilution factor. See explanation at the end of this chapter, page 88

* Parameters locked

Allow to locked a method parameters.

YES or NO. See explanation at the end of this chapter, page 91

NOTE: Three parameters (X axis, Y axis, type of curve) can be arbitrarily selected. The user can change them when calibration curve is done. For each parameter changing, the curve will be re drawn by holding account of the new parameter.

12.1.2 Impression of parameters

Press **F2 (Printer)** to print parameters.

12.1.3 Method saving

Press **F3 (Save)** to save method parameters.

12.1.4 Measure without sample blank

12.1.4.1 Measure with a factor

a) without blanc

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

F1-Execute F2-Parameters F3-File results Esc-Quit		2003/11/21 10:19:30
Concentration Mode v1.00		
PARAMETERS		
Type of measure	:	Abs
wavelength (nm):	:	500
Reagent blank	:	No
Sample blank	:	No
Decimal place (0-3):	:	1
No of standards (0-10):	:	0
Factor (+/-10000):	:	2.5
Unit	:	MG/L
Numbering	:	Auto
Parameters locked	:	No
Copyright SECOMAM SIMULATION		

* File results

See explanation of file results at the end of this chapter, page 86

NOTE: If the operator has failed to assign a name to a file for storing the data of a reading, the software creates a file by default call CONC.PRN. The data stored formerly will be overlaid by the new ones upon each reading.

Press **F1 (Execute)**. Enter the number of samples to be measured. Confirm.

F1-Measure F2-Simulation F3-Parameters Esc-Quit		2003/11/21 10:27:33
Concentration Mode v1.00		
CELL		RESULTS
CELL A Reference		Sample Conc. Abs.
CELL B Sam. 1		
CELL C Sam. 2		
CELL D Sam. 3		
CELL E Sam. 4		
CELL F Sam. 5		
CELL G Sam. 6		
CELL H Sam. 7		
CELL I Sam. 8		
Copyright SECOMAM SIMULATION		

* Simulation

This routine allows to enter by keyboard, absorbances of blank, standards and samples.

For explanation see at the end of this chapter, page 81

Prepare the multicell holder as indicated above.
Start measurement by pressing **F1 (Measure)**.

Enter number of cell (1-8):
2003/11/21 10:32:41

Concentration Mode v1.00

CELL	
CELL A	Reference
CELL B	Sam. 1
CELL C	Sam. 2
CELL D	Sam. 3
CELL E	Sam. 4
CELL F	Sam. 5
CELL G	Sam. 6
CELL H	Sam. 7
CELL I	Sam. 8

RESULTS			
Sample		Conc.	Abs.
Sam. 1		0.4 MG/L	0.173
Sam. 2		1.0 MG/L	0.381
Sam. 3		1.5 MG/L	0.610
Sam. 4		1.8 MG/L	0.739
Sam. 5		2.5 MG/L	0.989
Sam. 6		2.5 MG/L	1.019
Sam. 7		3.0 MG/L	1.192
Sam. 8		3.8 MG/L	1.514

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % _ () μ ± Enter

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ABSORBANCES DISPLAYED OF THE SAMPLES ARE READ AS AGAINST REFERENCE

The printing will be:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time : 10 :32 am
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method : Concentration Mode v1.00

Sam. 1	Conc.=	0.5 MG/L	Abs.= 0.185	Time: 10:32 am
Sam. 2	Conc.=	0.8 MG/L	Abs.= 0.320	
Sam. 3	Conc.=	1.4 MG/L	Abs.= 0.575	
Sam. 4	Conc.=	1.9 MG/L	Abs.= 0.751	
Sam. 5	Conc.=	2.0 MG/L	Abs.= 0.814	
Sam. 6	Conc.=	2.8 MG/L	Abs.= 1.102	Time: 10 :33 am
Sam. 7	Conc.=	3.4 MG/L	Abs.= 1.348	
Sam. 8	Conc.=	3.7 MG/L	Abs.= 1.476	
Sam. 9	Conc.=	3.0 MG/L	Abs.= 1.204	
Sam. 10	Conc.=	2.4 MG/L	Abs.= 0.973	

.....

The sample concentration will be calculated as follow:

$$Sam.Conc. = (Sam.Abs. - reference)Factor$$

(Values read against the air).

Enter number of samples to be measured. Confirm.

Follow indications displayed to prepare a new multicell holder for another series of measurement.

Press **F1 (Measure)** to read the following series.

Press **ESC** to leave the measuring mode.

b) With a blank

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

F1-Execute F2-Parameters F3-File results Esc-Quit 2003/11/21 11:11:29

Concentration Mode v1.00

PARAMETERS

Type of measure : Abs

wavelength (nm): 500
 Reagent blank : Yes
 Sample blank : No
 Decimal place (0-3): 1
 No of standards (0-10): 0
 Factor (+/-10000): 2.5
 Unit : MG/L
 Numbering : Auto
 Parameters locked : No

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Press **F1 (Execute)**. Enter the number of samples to be measured. Confirm.

F1-Measure F2-Simulation F3-Parameters Esc-Quit 2003/11/21 11:14:21

Concentration Mode v1.00

Sample RESULTS Conc. Abs.

CELL

CELL A Blank
 CELL B Sam. 1
 CELL C Sam. 2
 CELL D Sam. 3
 CELL E Sam. 4
 CELL F Sam. 5
 CELL G Sam. 6
 CELL H Sam. 7
 CELL I Sam. 8

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Prepare the multicell holder as indicated above.
 Start the reading by pressing **F1 (Measure)**.

Entrer number of cell (1-8): 2003/11/21 11:17:43

Concentration Mode v1.00

Sample RESULTS Conc. Abs.

CELL

CELL A Blank
 CELL B Sam. 1
 CELL C Sam. 2
 CELL D Sam. 3
 CELL E Sam. 4
 CELL F Sam. 5
 CELL G Sam. 6
 CELL H Sam. 7
 CELL I Sam. 8

Blank
 Sam. 1 0.5 MG/L 0.267
 Sam. 2 1.0 MG/L 0.204
 Sam. 3 1.3 MG/L 0.416
 Sam. 4 1.7 MG/L 0.532
 Sam. 5 2.1 MG/L 0.699
 Sam. 6 2.8 MG/L 0.833
 Sam. 7 3.3 MG/L 1.104
 Sam. 8 3.9 MG/L 1.320
 Sam. 8 3.9 MG/L 1.556

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
 Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () µ ± Enter

Copyright SECOMAM SIMULATION

THE DISPLAYED ABSORBANCES OF THE SAMPLES ARE READ AS AGAINST THE BLANK.
 THE DISPLAYED ABSORBANCE OF THE BLANK IS READ AS AGAINST AIR

The printing will be:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time : 10 :32 am
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method : Concentration Mode v1.00

Blank.....	Abs = 0.283	Time: 10:32 am
Sam. 1 Conc.= 0.5 MG/L	Abs.= 0.185	Time: 10:32 am
Sam. 2 Conc.= 0.8 MG/L	Abs.= 0.320	
Sam. 3 Conc.= 1.4 MG/L	Abs.= 0.575	
Sam. 4 Conc.= 1.9 MG/L	Abs.= 0.751	
Sam. 5 Conc.= 2.0 MG/L	Abs.= 0.814	
Sam. 6 Conc.= 2.8 MG/L	Abs.= 1.102	
Sam. 7 Conc.= 3.4 MG/L	Abs.= 1.348	
Sam. 8 Conc.= 3.7 MG/L	Abs.= 1.476	
Blank	Abs = 0.272	Time: 10:33 am
Sam. 9 Conc.= 3.0 MG/L	Abs.= 1.204	Time: 10:33 am
Sam. 10 Conc.= 2.4 MG/L	Abs.= 0.973	

The sample concentration will be calculated as follow:

$$Sam.Conc. = (Sam.Abs. - Blank)Factor$$

(Values read against the air).

Enter number of samples to be measured. Confirm.

Follow indications displayed to prepare a new multicell holder for another series of measurement.

Press **F1 (Measure)** to read the following series.

Press **ESC** to leave the measuring mode.

12.1.4.2 Measurement with a standard

a) without blanc

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

F1-Execute		F2-Parameters		F3-File results		Esc-Quit		2003/11/24 11:15:11	
Concentration Mode v1.00									
PARAMETERS									
Type of measure		Abs							
Wavelength (nm):		500							
Reagent blank :		No							
Sample blank :		No							
Decimal place (0-3):		1							
No of standards (0-10):		1							
Concentration(0-10000):		10.0							
Unit :		G/L							
Numbering :		Auto							
Parameters locked :		No							
Copyright SECOMAM SIMULATION									

Press **F1 (Execute)**.

F1-Measure **F2-Simulation** **F3-Parameters** **Esc-Quit** 2003/11/24 11:18:54

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A	Reference		
CELL B	Std.		
CELL C	Sam. 1		
CELL D	Sam. 2		
CELL E	Sam. 3		
CELL F	Sam. 4		
CELL G	Sam. 5		
CELL H	Sam. 6		
CELL I	Sam. 7		

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Prepare the multicell holder as indicated
Start the reading by pressing **F1 (Measure)**.

Enter number of cell (1-8): 2003/11/24 11:22:04

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
Std.	10.0 G/L	0.173	
Factor =	57.9		
Sam. 1	22.1 G/L	0.381	
Sam. 2	35.3 G/L	0.610	
Sam. 3	42.8 G/L	0.739	
Sam. 4	57.3 G/L	0.989	
Sam. 5	59.0 G/L	1.019	
Sam. 6	69.0 G/L	1.192	
Sam. 7	87.7 G/L	1.514	

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () μ ± Enter

Copyright SECOMAM **SIMULATION**

THE DISPLAYED ABSORBANCES OF THE STANDARD AND SAMPLES ARE READ AS AGAINST THE REFERENCE SOLUTION.

The results will be printed-out as follow:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
Date: Friday november the 21,2003 Time : 10 :32 am
User's name: SMITH
Batch number: 123
Origin: HOSPITAL
Kit number: 1256

Method : Concentration Mode v1.00

Std. Conc.= 10.0 G/L Abs.= 0.174 Time: 10:32 am
Factor = 57.5

Sam. 1	Conc.= 24.5 G/L	Abs.= 0.427	
Sam. 2	Conc.= 33.6 G/L	Abs.= 0.584	
Sam. 3	Conc.= 39.4 G/L	Abs.= 0.685	
Sam. 4	Conc.= 49.8 G/L	Abs.= 0.866	
Sam. 5	Conc.= 57.6 G/L	Abs.= 1.002	
Sam. 6	Conc.= 81.3 G/L	Abs.= 1.414	
Sam. 7	Conc.= 89.7 G/L	Abs.= 1.560	
Sam. 8	Conc.= 10.2 G/L	Abs.= 0.182	Time: 10:33 am
Sam. 9	Conc.= 19.2 G/L	Abs.= 0.342	

..... ..

The value of the factor is calculated as follow:

$$Factor = \frac{Std.Conc.}{Std.Abs. - reference}$$

The concentration of the sample is computed as follows:

$$Std.Conc. = (Sam.Abs. - reference)Factor$$

(Values read as against air).

Enter number of samples to be measured. Confirm.

Follow indications displayed to prepare a new multicell holder for another series of measurement.

Press **F1 (Measure)** to read the following series.

Press **ESC** to leave the measuring mode.

a) With blank

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

F1-Execute	F2-Parameters	F3-File results	Esc-Quit	2003/11/24 11:41:25																																	
Concentration Mode v1.00																																					
<table border="1"> <thead> <tr> <th colspan="3">PARAMETERS</th> </tr> </thead> <tbody> <tr> <td>Type of measure</td> <td>:</td> <td>Abs</td> </tr> <tr> <td>wavelength (nm):</td> <td>:</td> <td>500</td> </tr> <tr> <td>Reagent blank</td> <td>:</td> <td>Yes</td> </tr> <tr> <td>Sample blank</td> <td>:</td> <td>No</td> </tr> <tr> <td>Decimal place (0-3):</td> <td>:</td> <td>1</td> </tr> <tr> <td>No of standards (0-10):</td> <td>:</td> <td>1</td> </tr> <tr> <td>Concentration(0-10000):</td> <td>:</td> <td>10.0</td> </tr> <tr> <td>Unit</td> <td>:</td> <td>G/L</td> </tr> <tr> <td>Numbering</td> <td>:</td> <td>Auto</td> </tr> <tr> <td>Parameters locked</td> <td>:</td> <td>No</td> </tr> </tbody> </table>					PARAMETERS			Type of measure	:	Abs	wavelength (nm):	:	500	Reagent blank	:	Yes	Sample blank	:	No	Decimal place (0-3):	:	1	No of standards (0-10):	:	1	Concentration(0-10000):	:	10.0	Unit	:	G/L	Numbering	:	Auto	Parameters locked	:	No
PARAMETERS																																					
Type of measure	:	Abs																																			
wavelength (nm):	:	500																																			
Reagent blank	:	Yes																																			
Sample blank	:	No																																			
Decimal place (0-3):	:	1																																			
No of standards (0-10):	:	1																																			
Concentration(0-10000):	:	10.0																																			
Unit	:	G/L																																			
Numbering	:	Auto																																			
Parameters locked	:	No																																			
Copyright SECOMAM SIMULATION																																					

Press **F1 (Execute)**.

F1-Measure	F2-Simulation	F3-Parameters	Esc-Quit	2003/11/24 11:42:54																																												
Concentration Mode v1.00																																																
<table border="1"> <thead> <tr> <th colspan="2">CELL</th> <th colspan="2">RESULTS</th> </tr> <tr> <th>Sample</th> <th>Conc.</th> <th>Abs.</th> <th></th> </tr> </thead> <tbody> <tr> <td>CELL A Blank</td> <td></td> <td></td> <td></td> </tr> <tr> <td>CELL B Std.</td> <td></td> <td></td> <td></td> </tr> <tr> <td>CELL C Sam.</td> <td>1</td> <td></td> <td></td> </tr> <tr> <td>CELL D Sam.</td> <td>2</td> <td></td> <td></td> </tr> <tr> <td>CELL E Sam.</td> <td>3</td> <td></td> <td></td> </tr> <tr> <td>CELL F Sam.</td> <td>4</td> <td></td> <td></td> </tr> <tr> <td>CELL G Sam.</td> <td>5</td> <td></td> <td></td> </tr> <tr> <td>CELL H Sam.</td> <td>6</td> <td></td> <td></td> </tr> <tr> <td>CELL I Sam.</td> <td>7</td> <td></td> <td></td> </tr> </tbody> </table>					CELL		RESULTS		Sample	Conc.	Abs.		CELL A Blank				CELL B Std.				CELL C Sam.	1			CELL D Sam.	2			CELL E Sam.	3			CELL F Sam.	4			CELL G Sam.	5			CELL H Sam.	6			CELL I Sam.	7		
CELL		RESULTS																																														
Sample	Conc.	Abs.																																														
CELL A Blank																																																
CELL B Std.																																																
CELL C Sam.	1																																															
CELL D Sam.	2																																															
CELL E Sam.	3																																															
CELL F Sam.	4																																															
CELL G Sam.	5																																															
CELL H Sam.	6																																															
CELL I Sam.	7																																															
Copyright SECOMAM SIMULATION																																																

Prepare multicell holder as indicated.

Start reading by pressing **F1 (Measure)**.

Enter number of cell (1-8): 2003/11/24 11:45:13

Concentration Mode v1.00

CELL		RESULTS	
		Conc.	Abs.
CELL A	Blank		
CELL B	Std.		
CELL C	Sam. 1		
CELL D	Sam. 2		
CELL E	Sam. 3		
CELL F	Sam. 4		
CELL G	Sam. 5		
CELL H	Sam. 6		
CELL I	Sam. 7		

Blank			0.267
Std.	10.0 G/L		0.204
Factor = 49.1			
Sam. 1	20.4 G/L		0.416
Sam. 2	26.1 G/L		0.532
Sam. 3	34.3 G/L		0.699
Sam. 4	40.9 G/L		0.833
Sam. 5	54.2 G/L		1.104
Sam. 6	64.8 G/L		1.320
Sam. 7	76.4 G/L		1.556

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THE DISPLAYED ABSORBANCES OF THE STANDARD AND SAMPLES ARE READ AS AGAINST THE BLANK.
THE DISPLAYED ABSORBANCE OF THE BLANK IS READ AS AGAINST AIR.

The results will be print-out as follows:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time : 02:07 am
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method : Concentration Mode v1.00

Blank		Abs.= 0.050	Time: 02:07 pm
Std.	Conc.= 10.0 G/L	Abs.= 0.653	Time: 02:07 pm
Factor = 14.2			

Sam. 1	Conc.= 6.7 G/L	Abs.= 0.473	
Sam. 2	Conc.= 5.8 G/L	Abs.= 0.408	
Sam. 3	Conc.= 13.9 G/L	Abs.= 0.975	
Sam. 4	Conc.= 12.8 G/L	Abs.= 0.902	
Sam. 5	Conc.= 10.0 G/L	Abs.= 0.702	
Sam. 6	Conc.= 8.7 G/L	Abs.= 0.612	
Sam. 7	Conc.= 13.7 G/L	Abs.= 0.962	
Blank		Abs = 0.050	Time: 02:08 pm
Sam. 8	Conc.= 2.9 G/L	Abs.= 0.204	
Sam. 9	Conc.= 5.91 G/L	Abs.= 0.416	

The concentration value of the sample is calculated as follows:

$$Factor = \frac{Std.Conc.}{Std.Abs. - Blank}$$

The concentration of the sample is computed as follows:

$$Std.Conc. = (Sam.Abs. - Blank)Factor$$

Enter number of samples to be measured. Confirm.
 Follow indications displayed to prepare a new multicell holder for another series of measurement.
 Press **F1 (Measure)** to read the following series.
 Press **ESC** to leave the measuring mode.

12.1.4.3 Measurement with several standards

a) Preparing the measurement

We will not make any difference between the measurement with a blank or not. The displayed values on the curve are read as against the blank or reference solution.

Load the method or select "Concentration Mode".
Enter user's name, batch number, samples origin and reagent kit number.
Modify or programme parameters.
Save or not the method.

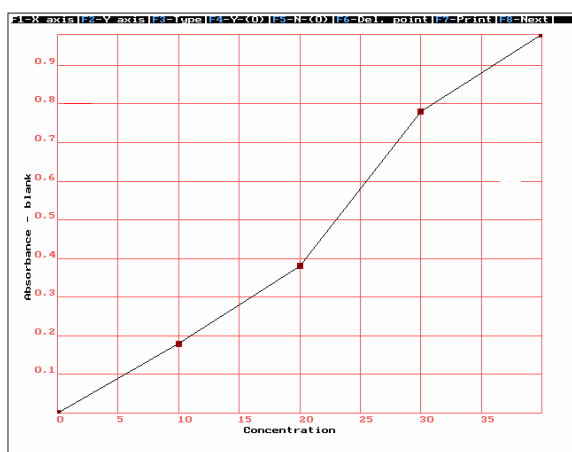
IMPORTANT: If the operator wants to keep the calibration curve, he must first of all save the method of analysis.

F1-Execute	F2-Parameters	F3-File results	Esc-Quit	2003/11/27 11:12:55
Concentration Mode v1.00				
PARAMETERS Type of measure Abs Wavelength (nm): 500 Reagent blank : Yes Sample blank : No Decimal place (0-3): 1 No of standards (0-10): 4 Conc. 1 (0-10000): 10.0 Conc. 2 (0-10000): 20.0 Conc. 3 (0-10000): 30.0 Conc. 4 (0-10000): 40.0 Unit : G/L X axis (Concentration): Lin Y axis (Absorbance): Lin Type of curve : Linear				
Copyright SECOMAM SIMULATION				

Press **F1 (Execute)**.

F1-Measure	F2-Simulation	F3-Parameters	Esc-Quit	2003/11/27 11:16:43																		
Concentration Mode v1.00																						
CELL CELL A Blank CELL B Std. 1 CELL C Std. 2 CELL D Std. 3 CELL E Std. 4 RESULTS <table border="1" style="width: 100%;"> <thead> <tr> <th>Sample</th> <th>Conc.</th> <th>Abs.</th> </tr> </thead> <tbody> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> </tbody> </table>					Sample	Conc.	Abs.															
Sample	Conc.	Abs.																				
Copyright SECOMAM SIMULATION																						

Prepare the multicell holder as indicated.
Start the reading by pressing **F1 (Measure)**.



b) Details on the curves and results

The curves are drawn from the standards and the zero-concentration point represented by the blank or the reference solution
The values displayed on the absorbance axis are the values of the standards or samples read as against the blank or the reference solution.

The curves will therefore go through zero. There are nonetheless two exceptions:

- In the event of a regression calculation with non-aligned calibration points.
- In the event of a logarithmic axis for absorbances or concentrations, the curve beginning at the first standard.

NOTE: The operator may also decide not to use the zero for calculating the curve if it is not exactly aligned with the calibration points (which is the case when standards have fairly high absorbances by reference to the zero and small absorbance differences between themselves).

The samples are read over a range between the absorbance of the zero standard – 10% (first standard for a logarithmic axis) and the absorbance of the last standard + 10%.

For samples not included in the above range, only the absorbances are displayed and the concentration is replaced by ****.

c) Change of curves parameters

When the data acquisition is over, the user has possibility to change the parameters.

- He can use or not the zero point for the curve calculation.
- He can change the X axis (concentration) or the Y axis (absorbance).
- He can change the type of calculation.
- He can eventually delete a calibration point.

Upon each change, the curve is redrawn in view of the new parameter.

See following pages for some examples.

For the explanations of different parameters (LOGIT axis, spline curve,...) see, at the end of this chapter page 80.

- Curve calculation without zero point

Press **F5 (N-(0))**.

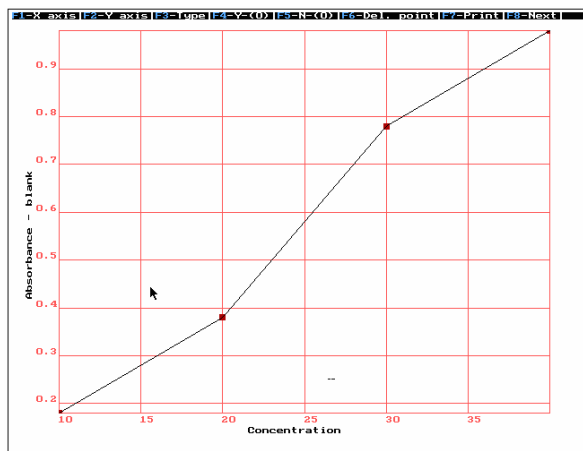
Example:

X-axis = Lin

Y-axis=Lin

Type = Linear

Zero point not used



Press **F4 (Y-(0))** to use the zero point again.

- Changing the X axis

Press **F1 (X-axis)**.

Choose a linear or logarithmic axis for concentrations

Press **F1 (Lin.)**: Linear axis for concentrations.

Press **F2 (Log.)**: Logarithmic axis for concentrations.

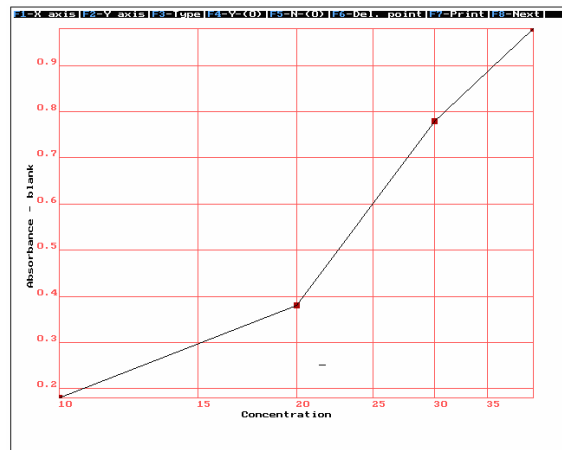
Example:

X-axis = Log.

Y-axis=Lin

Type = Linear

Zero point not used



- Changing the Y axis

Press **F2 (Y axis)**.

Choose a linear or logarithmic axis for absorbances or a calibrated axis in 1/Abs or Logit.

Press **F1 (Lin.)**: Linear axis for absorbances.

Press **F2 (Log.)**: Logarithmic axis for absorbances.

Press **F3 (1/Y)**: reverse of absorbance.

Press **F4 (Logit)**: See explanation in this chapter, page 80

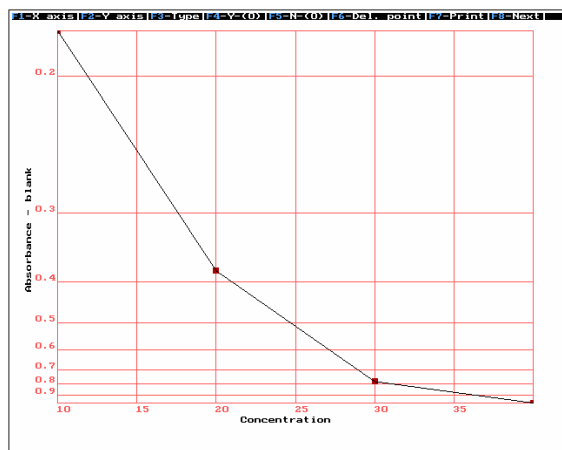
Example:

X-axis = Lin.

Y-axis=1/Y

Type = Linear

Zero point not used



- Changing the type of curve

Press **F3 (Type)**.

Choose among 4 types of curves

Press **F1 (Linear)**: line segments.

Press **F2 (Spline)**: spline curve.

Press **F3 (Regression.)**: linear regression curve.

Press **F4 (Regression.(0))**: linear regression going through the origin.

See explanation of different types of curve in this chapter, page 81

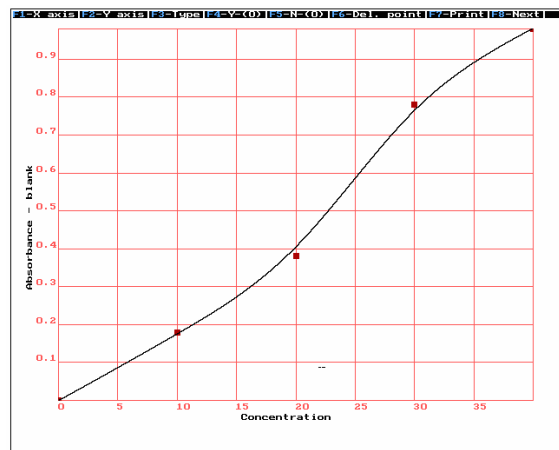
Example:

X-axis = Lin.

Y-axis=Lin.

Type = Spline

Zero point used



- Regression curve

It is possible to use two different types of curve for the regression mode:

- linear regression
- linear regression going through the origin

* Linear regression curve going through the origin

Press **F3 (Type)**.

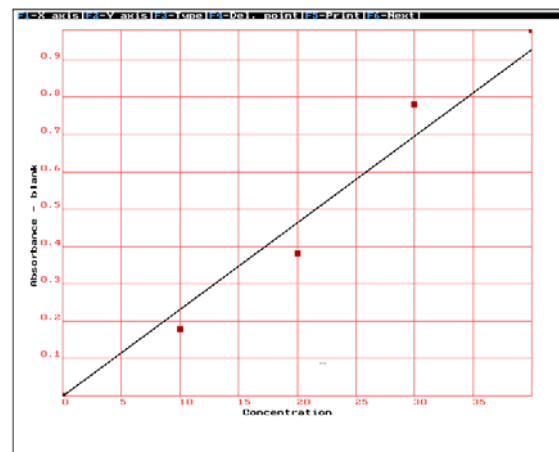
Press **F4 (Regression (0))**.

Example:

X-axis = Lin.

Y-axis=Lin.

Type = Regression (0)



* Regression linear curve

Press **F3 (Type)**.

Press **F3 (Regression)**.

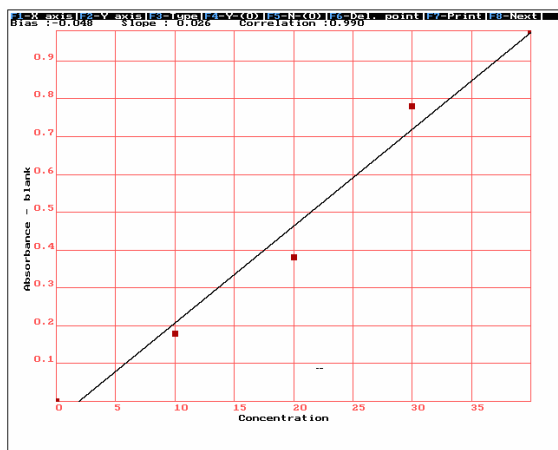
Example:

X-axis = Lin.

Y-axis=Lin.

Type = Regression

Zero point used



The spectrophotometer gives in the same time, with the linear regression curve, the three following parameters:

*** Bias**

Absorbance of the intersection point between the regression line and the Y axis.

*** Slope**

Slope of the regression line equal to $\frac{\delta Abs}{\delta Conc}$

*** Correlation**

The correlation coefficient is a number up to 1 which links the measuring points to the points of regression line. The closer it is to 1 the closer the measuring points will be to the points of the theoretical line.

REMARK

The axes of the calibration curve are graduated for absorbances and concentrations, whatever the type of axis selected (logarithmic, 1/Y,...)

But the ordinate at origin and the gradient of the regression line are computed according to the type of axis selected.

d) Point deletion

It is possible to delete one or several calibration points (maximum n-2, n being the number of standards measured) which have been poorly measured.

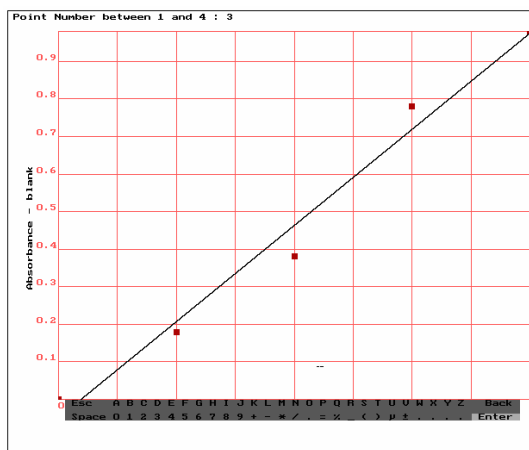
Upon each deletion, the software redraws the calibration curve in the previous configuration 'axes, calculation mode) but without the deleted point.

NOTE: The point deleted on the curve will be also deleted from the parameters of the method.

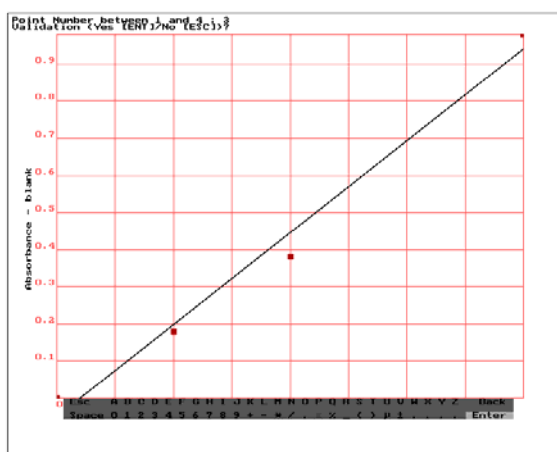
When the user load an analysis previous stored in memory, the deleted calibration points will be only for analysis in process and will not be in the methodology.

Example:

Press **F4 (Del.point)**.



Enter the calibration point number to be deleted and confirm.



Confirm or do not confirm such deletion.

The operation may be repeated n-2 times (n: number of calibration points).

e) Simulation

It is possible to enter the values of the blank and the standards with the keyboard.

They will be printed and displayed as the measures. See explanations in this chapter, page 81

f) Printing

For printing the calibration curve, press **F7 (Print)**.

g) Saving

The curve will automatically be saved if the user has already saved the analysis parameters.

h) Calibration anomalies

During the calibration curve setting up, it is possible that different anomaly messages are displayed. See explanation in this chapter, page 82

i) Recall a stored calibration curve

To recall a stored calibration curve, see, in this chapter, page 84

j) Measurement

Press F8 (Next) when calibration curve is over.

Enter the number of samples to be measured. Confirm.

F1-Measure F2-Simulation F3-Curve F4-Parameters Esc-Quit			
2003/12/01 11:01:19			
Concentration Mode v1.00			
CELL		RESULTS	
CELL A Blank		Sample	Conc.
CELL B Sam. 1		Blank	Abs.
CELL C Sam. 2		Std. 1	10.0 g/l 0.180
CELL D Sam. 3		Std. 2	20.0 g/l 0.380
CELL E Sam. 4		Std. 3	30.0 g/l 0.580
CELL F Sam. 5		Std. 4	40.0 g/l 0.780
CELL G Sam. 6			
CELL H Sam. 7			
CELL I Sam. 8			
Copyright SECOMAM SIMULATION			

Prepare the multicell holder as indicated.

Start the reading by pressing **F1 (Measure)**.

Enter number of cell (1-8): 2003/12/01 11:02:52

Concentration Mode v1.00

CELL		RESULTS	
		Conc.	Abs.
CELL A Blank			
CELL B Sam.	1		
CELL C Sam.	2		
CELL D Sam.	3		
CELL E Sam.	4		
CELL F Sam.	5		
CELL G Sam.	6		
CELL H Sam.	7		
CELL I Sam.	8		

Sample		Conc.	Abs.
Std.	1	10.0 g/l	0.180
Std.	2	20.0 g/l	0.380
Std.	3	30.0 g/l	0.580
Std.	4	40.0 g/l	0.780
Blank			0.270
Sam.	1	9.2 g/l	0.173
Sam.	2	19.9 g/l	0.381
Sam.	3	31.5 g/l	0.610
Sam.	4	38.1 g/l	0.739
Sam.	5	50.9 g/l	0.989
Sam.	6	52.4 g/l	1.019
Sam.	7	61.2 g/l	1.192
Sam.	8	77.7 g/l	1.514

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
 Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () μ ± Enter
 Copyright SECOMAM SIMULATION

THE DISPLAYED ABSORBANCES OF THE STANDARDS AND THE SAMPLES ARE READ AS AGAINST THE REFERENCE SOLUTION (without blank).

THE DISPLAYED ABSORBANCES OF THE STANDARDS AND THE SAMPLES ARE READ AS AGAINST THE BLANK (with a blank).

THE DISPLAYED ABSORBANCE OF THE BLANK IS READ AS AGAINST AIR.

The results will be printed out:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time : 02:21 pm
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method : Concentration Mode v1.00

Blank	Abs.= 0.020	Time: 02:21 pm
Std. 1 Conc.= 10.0 G/L	Abs.= 0.180	Time: 02:21 pm
Std. 2 Conc.= 20.0 G/L	Abs.= 0.380	
Std. 3 Conc.= 30.0 G/L	Abs.= 0.580	
Std. 4 Conc.= 40.0 G/L	Abs.= 0.780	

Bias = -0.008
 Slope = 0.020
 Correlation = 1.000

Blank	Abs.= 0.020	Time: 02:22 pm
Sam. 1 Conc.= 29.3 G/L	Abs.= 0.430	
Sam. 2 Conc.= 24.0 G/L	Abs.= 0.358	
Sam. 3 Conc.= 25.7 G/L	Abs.= 0.381	
Sam. 4 Conc.= 27.3 G/L	Abs.= 0.403	
Sam. 5 Conc.= 25.2 G/L	Abs.= 0.375	
Sam. 6 Conc.= 23.7 G/L	Abs.= 0.355	
Sam. 7 Conc.= 33.8 G/L	Abs.= 0.492	
Sam. 8 Conc.= 22.1 G/L	Abs.= 0.332	
Blanc	Abs.= 0.020	Time: 02:22 pm
Sam. 9 Conc.= 27.3 G/L	Abs.= 0.403	
Sam. 10 Conc.= 33.8 G/L	Abs.= 0.492	

.....

Enter number of samples to be measured. Confirm.

Follow indications displayed to prepare a new multicell holder for another series of measurement.

Press **F1 (Measure)** to read the following series.

Press **ESC** to leave the measuring mode.

12.1.5 Measurement with a sample blank

12.1.5.1 With a factor

a) Without blank

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

F1-Execute F2-Parameters F3-File results Esc-Quit 2003/12/01 11:51:47

Concentration Mode v1.00

PARAMETERS

Type of measure : Abs

Wavelength (nm):	500
Reagent blank :	No
Sample blank :	Yes
Decimal place (0-3):	1
No of standards (0-10):	0
Factor (+/-10000):	2.5
Unit :	G/L
Numbering :	Auto
Parameters locked :	No

Copyright SECOMAM SIMULATION

Press **F1 (Execute)**. Enter the number of samples to be measured. Confirm.

F1-Measure F2-Simulation F3-Parameters Esc-Quit 2003/12/01 11:53:26

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A Reference			
CELL B Sam. b1	1		
CELL C Sam.	1		
CELL D Sam. b1	2		
CELL E Sam.	2		
CELL F Sam. b1	3		
CELL G Sam.	3		
CELL H Sam. b1	4		
CELL I Sam.	4		

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Prepare the multicell holder as indicated.

Start the reading by pressing **F1 (Measure)**.

Enter number of cell (1-8): 2003/12/01 11:54:06

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A Reference			
CELL B Sam. b1	1		
CELL C Sam.	1		
CELL D Sam. b1	2		
CELL E Sam.	2		
CELL F Sam. b1	3		
CELL G Sam.	3		
CELL H Sam. b1	4		
CELL I Sam.	4		

Sam. b1	1		0.142
Sam.	1	0.4 G/L	0.315
Sam. b1	2		0.561
Sam.	2	0.5 G/L	0.764
Sam. b1	3		0.871
Sam.	3	0.5 G/L	1.090
Sam. b1	4		1.166
Sam.	4	1.1 G/L	1.591

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % _ () µ ± Enter

Copyright SECOMAM SIMULATION

THE DISPLAYED ABSORBANCES OF THE SAMPLE BLANKS AND SAMPLES ARE READ AS AGAINST THE REFERENCE SOLUTION.

The results will be printed out:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time: 11:43 am
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method : Concentration Mode v1.00

Sam.bl 1	Abs.= 0.186	Time: 11:43 am
Sam. 1 Conc.= 0.9 G/L	Abs.= 0.377	
Sam.bl 2	Abs.= 0.534	
Sam. 2 Conc.= 1.7 G/L	Abs.= 0.776	
Sam.bl 3	Abs.= 0.832	
Sam. 3 Conc.= 2.6 G/L	Abs.= 1.002	
Sam.bl 4	Abs.= 1.353	
Sam. 4 Conc.= 3.6 G/L	Abs.= 1.380	
Sam.bl 5	Abs.= 0.186	Time: 11:44 am
Sam. 5 Conc.= 0.9 G/L	Abs.= 0.377	
Sam.bl 6	Abs.= 0.534	
Sam. 6 Conc.= 1.7 G/L	Abs.= 0.776	

The concentration value of the sample is computed as follows:

$$Sam.Conc. = (Sam.Abs. - Sam.Bl)Factor$$

(Values read as against air).

Follow the instructions given on the screen to prepare the multicell older for another series.

Press **F1 (Measure)** to read the following series.

Press **ESC** to leave concentration mode.

b) With a blank

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

F1-Execute	F2-Parameters	F3-File results	Esc-Quit	2003/12/01 12:11:12																																	
Concentration Mode v1.00																																					
<table border="1"> <tr> <td colspan="3">PARAMETERS</td> </tr> <tr> <td>Type of measure</td> <td>:</td> <td>Abs</td> </tr> <tr> <td>wavelength (nm):</td> <td>:</td> <td>500</td> </tr> <tr> <td>Reagent blank</td> <td>:</td> <td>Yes</td> </tr> <tr> <td>Sample blank</td> <td>:</td> <td>Yes</td> </tr> <tr> <td>Decimal place (0-3):</td> <td>:</td> <td>1</td> </tr> <tr> <td>No of standards (0-10):</td> <td>:</td> <td>0</td> </tr> <tr> <td>Factor (+/-10000):</td> <td>:</td> <td>2.5</td> </tr> <tr> <td>Unit</td> <td>:</td> <td>G/L</td> </tr> <tr> <td>Numbering</td> <td>:</td> <td>Auto</td> </tr> <tr> <td>Parameters locked</td> <td>:</td> <td>No</td> </tr> </table>					PARAMETERS			Type of measure	:	Abs	wavelength (nm):	:	500	Reagent blank	:	Yes	Sample blank	:	Yes	Decimal place (0-3):	:	1	No of standards (0-10):	:	0	Factor (+/-10000):	:	2.5	Unit	:	G/L	Numbering	:	Auto	Parameters locked	:	No
PARAMETERS																																					
Type of measure	:	Abs																																			
wavelength (nm):	:	500																																			
Reagent blank	:	Yes																																			
Sample blank	:	Yes																																			
Decimal place (0-3):	:	1																																			
No of standards (0-10):	:	0																																			
Factor (+/-10000):	:	2.5																																			
Unit	:	G/L																																			
Numbering	:	Auto																																			
Parameters locked	:	No																																			
Copyright SECOMAM SIMULATION																																					

Press **F1 (Execute)**. Confirm.

F1-Measure F2-Simulation F3-Parameters Esc-Quit 2003/12/01 12:12:28

Concentration Mode v1.00

CELL	Sample	RESULTS Conc.	Abs.
CELL A Reference			
CELL B Blank b1			
CELL C Blank			

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Prepare the multicell holder as indicated.
Start the reading by pressing **F1 (Measure)**.

Enter number of cell (1-8): 8 2003/12/01 12:14:30

Concentration Mode v1.00

CELL	Sample	RESULTS Conc.	Abs.
CELL A Reference			
CELL B Blank b1	Blank b1		0.183
CELL C Blank	Blank		0.344

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % _ () μ ± Enter

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Enter the number of samples to be measured. Confirm.

F1-Measure F2-Simulation F3-Parameters Esc-Quit 2003/12/01 12:18:55

Concentration Mode v1.00

CELL	Sample	RESULTS Conc.	Abs.
CELL A Reference			
CELL B Sam. b1 1	Blank b1		0.183
CELL C Sam. 1	Blank		0.344
CELL D Sam. b1 2			
CELL E Sam. 2			
CELL F Sam. b1 3			
CELL G Sam. 3			
CELL H Sam. b1 4			
CELL I Sam. 4			

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Prepare the multicell holder as indicated.
Start the reading by pressing **F1 (Measure)**.

Enter number of cell (1-8): 2003/12/01 12:24:04

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A Reference			
CELL B Sam. b1	1		
CELL C Sam.	1	0.1 G/L	0.377
CELL D Sam. b1	2		0.524
CELL E Sam.	2	0.1 G/L	0.741
CELL F Sam. b1	3		0.839
CELL G Sam.	3	0.4 G/L	1.171
CELL H Sam. b1	4		1.420
CELL I Sam.	4	*****	1.577

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () μ ± Enter

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THE DISPLAYED ABSORBANCES OF THE SAMPLES, SAMPLE BLANKS AND BLANK OF THE BLANK ARE READ AS AGAINST THE REFERENCE SOLUTION.

The results will be printed out:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time: 11:43 am
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method : Concentration Mode v1.00

Blank bl	Abs.= 0.185	Time: 11:43 am
Blank	Abs.= 0.320	
Sam.bl 1	Abs.= 0.161	Time: 11:45 am
Sam. 1 Conc.= 0.1 G/L	Abs.= 0.355	
Sam.bl 2	Abs.= 0.594	
Sam. 2 Conc.= 0.1 G/L	Abs.= 0.776	
Sam.bl 3	Abs.= 0.866	
Sam. 3 Conc.= 0.3 G/L	Abs.= 1.102	
Sam.bl 4	Abs.= 1.270	
Sam. 4 Conc.= 0.4 G/L	Abs.= 1.546	
Sam.bl 5	Abs.= 0.161	Time: 11:47 am
Sam. 5 Conc.= 0.1 G/L	Abs.= 0.355	
Sam.bl 6	Abs.= 0.594	
Sam. 6 Conc.= 0.1 G/L	Abs.= 0.776	

..... ..

The concentration value of the sample is computed as follows:

$$Sam.Conc. = [(Sam.Abs. - Sam.Bl.) - (Blank - Bl.Blank)] Factor$$

(Values read as against air).

Follow the instructions given on the screen to prepare the multicell older for another series.

Press **F1 (Measure)** to read the following series.
 Press **ESC** to leave concentration mode.

12.1.5.2 With a standard

a) Without a blank

Load the method or select "Concentration Mode".
 Enter user's name, batch number, samples origin and reagent kit number.
 Modify or programme parameters.
 Save or not the method.

F1-Execute F2-Parameters F3-File results Esc-Quit 2003/12/01 15:08:54

Concentration Mode v1.00

PARAMETERS

Type of measure : Abs

Wavelength (nm):	500
Reagent blank :	No
Sample blank :	Yes
Decimal place (0-3):	1
No of standards (0-10):	1
Concentration(0-10000):	10.0
Unit :	G/L
Numbering :	Auto
Parameters locked :	No

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Press **F1 (Execute)**.

F1-Measure F2-Simulation F3-Parameters Esc-Quit 2003/12/01 15:23:47

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A Reference			
CELL B Std. b1			
CELL C Std.			
CELL D Sam. b1	1		
CELL E Sam.	1		
CELL F Sam. b1	2		
CELL G Sam.	2		
CELL H Sam. b1	3		
CELL I Sam.	3		

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Prepare the multicell holder as indicated.
Start the reading by pressing **F1 (Measure)**.

Entrer number of cell (1-8): 2003/12/01 15:26:55

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A Reference			
CELL B Std. b1			
CELL C Std.			
CELL D Sam. b1	1		
CELL E Sam.	1		
CELL F Sam. b1	2		
CELL G Sam.	2		
CELL H Sam. b1	3		
CELL I Sam.	3		

Std. b1		0.175
Std.	10.0 G/L	0.390
Factor =	46.6	
Sam. b1	1	0.558
Sam.	1 11.1 G/L	0.796
Sam. b1	2	0.894
Sam.	2 5.8 G/L	1.017
Sam. b1	3	1.230
Sam.	3 11.7 G/L	1.482

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () µ ± Enter

Copyright SECOMAM **SIMULATION**

THE DISPLAYED ABSORBANCES OF THE SAMPLES, STANDARD, SAMPLE BLANC AND BLANK OF THE BLANK ARE READ AS AGAINST THE REFERENCE SOLUTION.

The results will be printed-out:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time: 11:43 am
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method : Concentration Mode v1.00

Std.bl. Abs.= 0.183 Time: 11:43 am
 Std. Conc.= 10.0 G/L Abs.= 0.352 Time: 11:43 am
 Factor = 59.1

Sam.bl 1 Abs.= 0.578
 Sam. 1 Conc.= 0.1 G/L Abs.= 0.651
 Sam.bl 2 Abs.= 0.845
 Sam. 2 Conc.= 0.1 G/L Abs.= 1.144
 Sam.bl 3 Abs.= 1.282
 Sam. 3 Conc.= 0.3 G/L Abs.= 1.520
 Sam.bl 4 Abs.= 0.845 Time: 11:45 am
 Sam. 4 Conc.= 0.1 G/L Abs.= 1.144
 Sam.bl 5 Abs.= 1.282
 Sam. 5 Conc.= 0.3 G/L Abs.= 1.520

The value of the factor is calculated as follows:

$$Factor = \frac{Std.Conc.}{Std.Abs. - Std.Bl.}$$

(Values read as against air).

The concentration of the sample is:

$$Sam.Conc. = (Sam.Abs. - Sam.Bl.)Factor$$

(Values read as against air).

Enter the number of samples to be measured. Confirm.

Follow the instructions given on the screen to prepare the multicell older for another series.

Press **F1 (Measure)** to read the following series.

Press **ESC** to leave concentration mode.

b) With a blank

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

F1-Execute		F2-Parameters		F3-File results		Esc-Quit		2003/12/01 15:53:59	
Concentration Mode v1.00									
PARAMETERS									
Type of measure	:	Abs							
wavelength (nm):	:	500							
Reagent blank	:	Yes							
Sample blank	:	Yes							
Decimal place (0-3):	:	1							
No of standards (0-10):	:	1							
Concentration(0-10000):	:	10.0							
Unit	:	G/L							
Numbering	:	Auto							
Parameters locked	:	No							
Copyright SECOMAM SIMULATION									

Press **F1 (Execute)**.

F1-Measure F2-Simulation F3-Parameters Esc-Quit 2003/12/01 15:55:24

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A Reference			
CELL B Blank b1			
CELL C Std. b1			
CELL D Blank			
CELL E Std.			
CELL F Sam. b1	1		
CELL G Sam.	1		
CELL H Sam. b1	2		
CELL I Sam.	2		

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Prepare the multicell holder as indicated.
Start the reading by pressing **F1 (Measure)**.

Enter number of cell (1-8): 2003/12/01 16:08:17

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A Reference			
CELL B Blank b1		0.010	
CELL C Std. b1		0.047	
CELL D Blank		0.030	
CELL E Std.		0.543	
CELL F Sam. b1	1		
CELL G Sam.	1		
CELL H Sam. b1	2		
CELL I Sam.	2		

Sample	Conc.	Abs.
Blank b1		0.010
Std. b1		0.047
Blank		0.030
Std.	10.0 G/L	0.543
Factor =	21.0	
Sam. b1	1	0.030
Sam.	1 8.2 G/L	0.438
Sam. b1	2	0.035
Sam.	2 9.2 G/L	0.492

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () µ ± Enter

Copyright SECOMAM SIMULATION

THE DISPLAYED ABSORBANCES OF THE SAMPLES, STANDARD, BLANK, SAMPLE BLANKS, STANDARD BLANK AND BLANK OF THE BLANK ARE READ AS AGAINST THE REFERENCE

The results will be printed-out:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
Date: Friday november the 21,2003 Time: 11:43 am
User's name: SMITH
Batch number: 123
Origin: HOSPITAL
Kit number: 1256

Method : Concentration Mode v1.00

Blank bl	Abs.= 0.010	Time: 11:43 am
Std. bl	Abs.= 0.047	
Blank	Abs.= 0.030	
Std. Conc.= 10.0 G/L	Abs.= 0.543	Time: 11:43 am
Factor = 21.0		
Sam.bl 1	Abs.= 0.030	
Sam. 1 Conc.= 8.2 G/L	Abs.= 0.438	
Sam.bl 2	Abs.= 0.035	
Sam. 2 Conc.= 9.2 G/L	Abs.= 0.492	
Sam.bl 3	Abs.= 0.072	Time: 11:45 am
Sam. 3 Conc.= 10.7 G/L	Abs.= 0.589	
Sam.bl 4	Abs.= 0.074	
Sam. 4 Conc.= 19.6 G/L	Abs.= 1.009	

..... ..

If when result is displayed, it appears *****, it means that the result of the calculation, before multiplication by factor, is negative.
The factor is calculated as follows:

$$Factor = \frac{Std.Conc.}{(Std.Abs. - Std.Bl.) - (Blank - Bl.Blank)}$$

(Values read as against the air).

The concentration of the sample is:

$$SamConc = [(SamAbs - SamBl.) - (Blank - Bl.Blank)] Factor$$

(Values read as against the air).

Enter the number of samples to be measured. Confirm.

Follow the instructions given on the screen to prepare the multicell older for another series.

Press **F1 (Measure)** to read the following series.

Press **ESC** to leave concentration mode.

12.1.5.3 Measurement with several standards

a) Without reagent blank

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

IMPORTANT: If the operator wants to keep the calibration curve, he must first of all save the method of analysis.

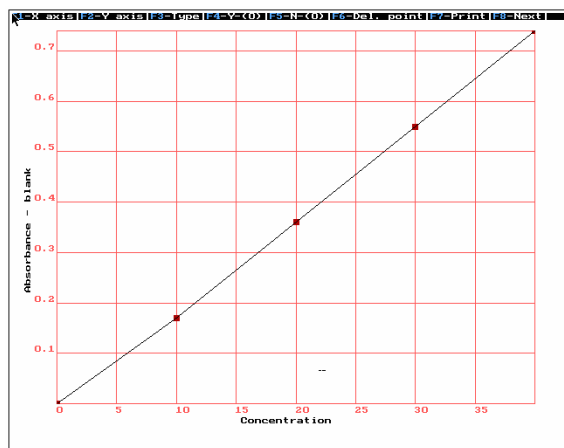
F1-Execute	F2-Parameters	F3-File results	Esc-Quit	2003/12/01 16:49:10
Concentration Mode v1.00				
PARAMETERS Type of measure : Abs Sample blank : Yes Decimal place (0-3): 1 No of standards (0-10): 4 Conc. 1 (0-10000) : 10.0 Conc. 2 (0-10000) : 20.0 Conc. 3 (0-10000) : 30.0 Conc. 4 (0-10000) : 40.0 Unit : g/l X axis (Concentration): Lin Y axis (Absorbance): Lin Type of curve : Linear Numbering : Auto Parameters locked : No				
Copyright SECOMAM SIMULATION				

Press **F1 (Execute)**.

F1-Measure	F2-Simulation	F3-Parameters	Esc-Quit	2003/12/01 16:50:53																														
Concentration Mode v1.00																																		
CELL CELL A Reference CELL B Std. b1 1 CELL C Std. b1 2 CELL D Std. b1 3 CELL E Std. b1 4 CELL F Std. 1 CELL G Std. 2 CELL H Std. 3 CELL I Std. 4 RESULTS <table style="width: 100%;"> <thead> <tr> <th>Sample</th> <th>Conc.</th> <th>Abs.</th> </tr> </thead> <tbody> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> </tbody> </table>					Sample	Conc.	Abs.																											
Sample	Conc.	Abs.																																
Copyright SECOMAM SIMULATION																																		

Prepare the multicell holder as indicated.

Start the reading by pressing **F1 (Measure)**.



* DETAILS ON THE CURVE

The values displayed on the absorbance axis are the values of the standards or samples calculated as follows:

$$\text{Displayed Abs.} = \text{Abs.}(\text{Std. or Sam.}) - \text{Bl.}(\text{Std. or Sam.})$$

(Values read as against the air).

Refer, in this chapter, to the page 81. for the processing of the curve (How to change the curve axis, point deletion,...)

Press **F8** when the calibration curve is over.

Enter the number of samples to be measured. Confirm.

Entrer number of cell (1-8):

Concentration Mode v1.00

CELL	Reference
CELL A	Reference
CELL B	Std. b1 1
CELL C	Std. b1 2
CELL D	Std. b1 3
CELL E	Std. b1 4
CELL F	Std. 1
CELL G	Std. 2
CELL H	Std. 3
CELL I	Std. 4

Sample	Conc.	Abs.
Std. b1	1	0.010
Std. b1	2	0.020
Std. b1	3	0.030
Std. b1	4	0.040
Std. 1	10.0 g/l	0.180
Std. 2	20.0 g/l	0.380
Std. 3	30.0 g/l	0.580
Std. 4	40.0 g/l	0.780

Esc ABCDEFGHIJKL MNOPQRSTUVWXYZ Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () μ ± Enter

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Prepare the multicell holder as indicated.

Start the reading by pressing **F (Measure)**.

Entrer number of cell (1-8):

Concentration Mode v1.00

CELL	Reference
CELL A	Reference
CELL B	Sam. b1 1
CELL C	Sam. 1
CELL D	Sam. b1 2
CELL E	Sam. 2
CELL F	Sam. b1 3
CELL G	Sam. 3
CELL H	Sam. b1 4
CELL I	Sam. 4

Sample	Conc.	Abs.
Std. b1	4	0.040
Std. 1	10.0 g/l	0.180
Std. 2	20.0 g/l	0.380
Std. 3	30.0 g/l	0.580
Std. 4	40.0 g/l	0.780
Sam. b1	1	0.194
Sam. 1	11.1 g/l	0.385
Sam. b1	2	0.550
Sam. 2	11.4 g/l	0.747
Sam. b1	3	0.988
Sam. 3	5.8 g/l	1.087
Sam. b1	4	1.368
Sam. 4	*****	1.311

Esc ABCDEFGHIJKL MNOPQRSTUVWXYZ Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () μ ± Enter

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THE DISPLAYED ABSORBANCES OF THE SAMPLES, STANDARDS, SAMPLE BLANKS AND STANDARDS BLANKS ARE READ AS AGAINST THE REFERENCE SOLUTION.

The results will be printed-out:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00			
Date: Friday november the 21,2003 Time: 11:43 am			
User's name: SMITH			
Batch number: 123			
Origin: HOSPITAL			
Kit number: 1256			
Method : Concentration Mode v1.00			
Std. bl.	1	Abs.= 0.102	Time: 11:43 am
Std. bl.	2	Abs.= 0.120	
Std. bl.	3	Abs.= 0.115	
Std. bl.	4	Abs.= 0.099	
Std.	1 Conc.= 10.0 G/L	Abs.= 0.200	
Std.	2 Conc.= 20.0 G/L	Abs.= 0.400	
Std.	3 Conc.= 30.0 G/L	Abs.= 0.600	
Std.	4 Conc.= 40.0 G/L	Abs.= 0.750	
Bias	= -0.035		
Slope	= 0.017		
Correlation	= 0.994		
Sam. bl	1	Abs.= 0.228	Time: 11:45 am
Sam.	1 Conc.= 0.1 G/L	Abs.= 0.400	
Sam. bl	2	Abs.= 0.568	
Sam.	2 Conc.= 0.1 G/L	Abs.= 0.737	
Sam. bl	3	Abs.= 0.859	
Sam.	3 Conc.= 0.3 G/L	Abs.= 1.071	
Sam. bl	4	Abs.= 1.208	
Sam.	4 Conc.= 0.4 G/L	Abs.= 1.585	
.....			

Enter the number of samples to be measured. Confirm.

Follow the instructions given on the screen to prepare the multicell older for another series.

Press **F1 (Measure)** to read the following series.

Press **ESC** to leave concentration mode.

b) With a blank

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

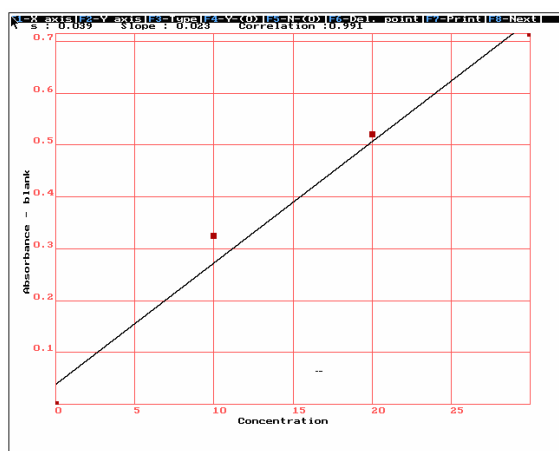
IMPORTANT: If the operator wants to keep the calibration curve, he must first of all save the method of analysis.

F1-Execute	F2-Parameters	F3-File results	Esc-Quit	2003/12/01 17:31:30																														
Concentration Mode v1.00																																		
<table border="1"> <tr> <td colspan="2">PARAMETERS</td> </tr> <tr> <td>Type of measure</td> <td>: Abs</td> </tr> <tr> <td>Reagent blank</td> <td>: Yes</td> </tr> <tr> <td>Sample blank</td> <td>: Yes</td> </tr> <tr> <td>Decimal place (0-3):</td> <td>1</td> </tr> <tr> <td>No of standards (0-10):</td> <td>3</td> </tr> <tr> <td>Conc. 1 (0-10000):</td> <td>10.0</td> </tr> <tr> <td>Conc. 2 (0-10000):</td> <td>20.0</td> </tr> <tr> <td>Conc. 3 (0-10000):</td> <td>30.0</td> </tr> <tr> <td>Unit</td> <td>: g/l</td> </tr> <tr> <td>X axis (Concentration):</td> <td>Lin</td> </tr> <tr> <td>Y axis (Absorbance):</td> <td>Lin</td> </tr> <tr> <td>Type of curve</td> <td>: Regre</td> </tr> <tr> <td>Numbering</td> <td>: Auto</td> </tr> <tr> <td>Parameters locked</td> <td>: No</td> </tr> </table>					PARAMETERS		Type of measure	: Abs	Reagent blank	: Yes	Sample blank	: Yes	Decimal place (0-3):	1	No of standards (0-10):	3	Conc. 1 (0-10000):	10.0	Conc. 2 (0-10000):	20.0	Conc. 3 (0-10000):	30.0	Unit	: g/l	X axis (Concentration):	Lin	Y axis (Absorbance):	Lin	Type of curve	: Regre	Numbering	: Auto	Parameters locked	: No
PARAMETERS																																		
Type of measure	: Abs																																	
Reagent blank	: Yes																																	
Sample blank	: Yes																																	
Decimal place (0-3):	1																																	
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Y axis (Absorbance):	Lin																																	
Type of curve	: Regre																																	
Numbering	: Auto																																	
Parameters locked	: No																																	
Copyright SECOMAM SIMULATION																																		

Press **F1 (Execute)**.

F1-Measure	F2-Simulation	F3-Parameters	Esc-Quit	2003/12/02 07:36:12																														
Concentration Mode v1.00																																		
CELL CELL A Reference CELL B Blank b1 CELL C Std. b1 1 CELL D Std. b1 2 CELL E Std. b1 3 CELL F Blank CELL G Std. 1 CELL H Std. 2 CELL I Std. 3		RESULTS <table border="1"> <thead> <tr> <th>Sample</th> <th>Conc.</th> <th>Abs.</th> </tr> </thead> <tbody> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> <tr><td> </td><td> </td><td> </td></tr> </tbody> </table>			Sample	Conc.	Abs.																											
Sample	Conc.	Abs.																																
Copyright SECOMAM SIMULATION																																		

Prepare the multicell holder as indicated.
Start reading by pressing **F1 (Measure)**.



* DETAILS ON THE CURVE

The values displayed on the absorbance axis are the values of the standards or samples calculated as follows:

$$Displ.Abs. = [Abs.(Std.or.Sam.) - Bl.(Std.or.Sam.)] - (Blank - Bl.Blank)$$

(Values read as against the air).

Press **F8** when the calibration curve is over.
Enter the number of samples to be measured. Confirm.

F1-Measure	F2-Simulation	F3-Curve	F4-Parameters	Esc-Quit	2003/12/02 08:02:48																											
Concentration Mode v1.00																																
CELL CELL A Reference CELL B Sam. b1 1 CELL C Sam. 1 CELL D Sam. b1 2 CELL E Sam. 2 CELL F Sam. b1 3 CELL G Sam. 3 CELL H Sam. b1 4 CELL I Sam. 4		RESULTS <table border="1"> <thead> <tr> <th>Sample</th> <th>Conc.</th> <th>Abs.</th> </tr> </thead> <tbody> <tr><td>Blank b1</td><td> </td><td>0.020</td></tr> <tr><td>Std. b1 1</td><td>1</td><td>0.035</td></tr> <tr><td>Std. b1 2</td><td>2</td><td>0.040</td></tr> <tr><td>Std. b1 3</td><td>3</td><td>0.045</td></tr> <tr><td>Blank</td><td> </td><td>0.060</td></tr> <tr><td>Std. 1</td><td>10.0 G/L</td><td>0.400</td></tr> <tr><td>Std. 2</td><td>20.0 G/L</td><td>0.600</td></tr> <tr><td>Std. 3</td><td>30.0 G/L</td><td>0.800</td></tr> </tbody> </table>				Sample	Conc.	Abs.	Blank b1		0.020	Std. b1 1	1	0.035	Std. b1 2	2	0.040	Std. b1 3	3	0.045	Blank		0.060	Std. 1	10.0 G/L	0.400	Std. 2	20.0 G/L	0.600	Std. 3	30.0 G/L	0.800
Sample	Conc.	Abs.																														
Blank b1		0.020																														
Std. b1 1	1	0.035																														
Std. b1 2	2	0.040																														
Std. b1 3	3	0.045																														
Blank		0.060																														
Std. 1	10.0 G/L	0.400																														
Std. 2	20.0 G/L	0.600																														
Std. 3	30.0 G/L	0.800																														
Copyright SECOMAM SIMULATION																																

Prepare the multicell holder as indicated.
Start reading by pressing **F1 (Measure)**.

Enter number of cell (1-8): 2003/12/02 08:04:37

Concentration Mode v1.00

CELL		RESULTS	
CELL	Reference	Sample	Abs.
CELL A	Reference	Std. b1	3
CELL B	Sam. b1	Blank	
CELL C	Sam. 1	Std. 1	10.0 G/L
CELL D	Sam. b1	Std. 2	20.0 G/L
CELL E	Sam. 2	Std. 3	30.0 G/L
CELL F	Sam. b1	Sam. b1	1
CELL G	Sam. 3	Sam. 1	5.5 G/L
CELL H	Sam. b1	Sam. b1	2
CELL I	Sam. 4	Sam. 2	2.1 G/L
		Sam. b1	3
		Sam. 3	*****
		Sam. b1	4
		Sam. 4	10.4 G/L

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THE DISPLAYED ABSORBANCES OF THE SAMPLES, STANDARDS, BLANK, SAMPLE BLANKS, STANDARDS BLANKS AND BLANK OF THE BLANK ARE READ AS AGAINST THE REFERENCE SOLUTION.

The results will be printed-out:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time: 11:43 am
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method : Concentration Mode v1.00

Blank Bl	Abs.= 0.052	Time: 11:43 am
Std.bl. 1	Abs.= 0.100	
Std.bl. 2	Abs.= 0.095	
Std.bl. 3	Abs.= 0.107	
Blank	Abs.= 0.075	
Std. 1 Conc.= 10.0 G/L	Abs.= 0.300	
Std. 2 Conc.= 20.0 G/L	Abs.= 0.600	
Std. 3 Conc.= 30.0 G/L	Abs.= 0.850	
Bias	= -0.025	
Slope	= 0.025	
Correlation	= 0.995	
Sam.bl. 1	Abs.= 0.191	Time: 11:47 am
Sam. 1 Conc.= 6.9 G/L	Abs.= 0.359	
Sam.bl. 2	Abs.= 0.564	
Sam. 2 Conc.= 4.6 G/L	Abs.= 0.676	
Sam.bl. 3	Abs.= 0.985	
Sam. 3 Conc.= 8.3 G/L	Abs.= 1.188	
Sam.bl. 4	Abs.= 1.337	
Sam. 4 Conc.= *****	Abs.= 1.318	

***** Means that the calculation (*Sam. – Sam.Bl.*) before to be reported on Y axis is negative.

Enter the number of samples to be measured. Confirm.
 Follow the instructions given on the screen to prepare the multicell older for another series.
 Press **F1 (Measure)** to read the following series.
 Press **ESC** to leave concentration mode.

12.2 CALIBRATED KINETIC

This measuring method also called 2-point kinetic method (2ptskin) allows to calculate the absorbance variation of a solution as a function of time.

As a rule, the result is as follows:

$$R = \frac{(Abs.t_1 - Abs.t_2) \times Factor \times 60}{tm}$$

Abs.t₁ : Abs of the solution at the end of the lag time.

Abs.t₂ : Abs of the solution at the end of the measuring time.

Factor : Coefficient of molecular absorption.

tm : Measuring time.

$\frac{60}{tm}$: Ratio reducing the result to one minute.

But the results can also be given in comparison with a standard or a calibration range.

12.2.1 Programming the parameters

For the parameters modification, see page 36

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

Concentration Mode v1.00

PARAMETERS

Type of measure : 2ptsKin

Wavelength (nm): 500
 Lag time (0-2000s): 5
 Meas. time (20-10000s): 30
 Reagent blank : No
 Decimal place (0-3): 1
 No of standards (0-10): 3
 Conc. 1 (0-10000) : 10.0
 Conc. 2 (0-10000) : 20.0
 Conc. 3 (0-10000) : 30.0
 Unit : g/l
 X axis (Concentration): Lin
 Y axis (Absorbance): Lin
 Type of curve : Regre

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* Type of measurement

Choose 2ptsKin (2 points kinetic)

* Wavelength

Between 190 and 900 nm

* Lag time

from 0 to 2000 seconds of time

The lag time is introduced at the beginning of the reading to take into account the non-linearity of a solution. The unit performs the reading in the meantime but the delta of absorbance will only be calculated at the end of such time.

* Measuring time

from 20 to 10000 seconds

* Reagent blank

YES or NO (See meaning of the blank in this chapter, page 80)

* Decimal place

from 0 to 3

This parameter defines the number of significant digits after the decimal point.

* Number of standards

Factor

To work with a factor, answer 0.
Choose a value between +/- 10000.

1 standard

To work with 1 standard, answer 1.
Choose a value between 0 and 10000.

Several standards

To work with several standards, enter the number of standards (from 2 through 10).
Choose a value between 0 and 10000.

* Unit

With keyboard, enter the abbreviation wanted.

* X axis (Concentration axis)

Choose between linear and logarithmic

* Y axis (Absorbance axis)

Linear, logarithmic, 1/Abs (1/Y) or Logit. . See Logit axis meaning at the end of this chapter page 80

* Type of curve

Linear (segmented curve), "Regre" (linear regression), "Regre (0)" (linear regression going through the origin 0), Spline. See explanation on the type of curve at the end of this chapter page 81

* Numbering

This parameter concerns samples identification.

Auto: Identification of the sample is numerical and increasing.

Example: Sam.1, Sam.2,...

Unit: The user assigns a name to each sample (8 characters) and eventually attributes a dilution factor. See explanation at the end of this chapter, page 88

Table: The user prepares a table in which he will enter the number of samples, their name, and the dilution factor. See explanation at the end of this chapter, page 88

* Parameters locked

Allow to locked a method parameters.

YES or NO. See explanation at the end of this chapter, page 73

NOTE: Three parameters (X axis, Y axis, type of curve) can be arbitrarily selected. The user can change them when calibration curve is done. For each parameter changing, the curve will be re drawn by holding account of the new parameter.

12.2.2 Impression of parameters

Press **F2 (Printer)** to print parameters.

12.2.3 Method saving

Press **F3 (Save)** to save method parameters.

12.2.4 Measurement

During measurement, on the top of the screen, will be displayed the count down of the total measuring time.

The procedure for these measurements is the same as for those performed in the concentration mode. The difference will lie in the way of interpreting the readings and the results.

12.2.5 The readings

The delta of absorbance will be measured by reference to air or by reference to a delta of the blank.

12.2.6 The results

They are expressed as follows:

$$Sam.Conc. = (\Delta Abs / mn\_Sam. - \Delta Abs. / mn\_Blank) Factor$$

If there is a standard, the factor will be calculated as follows :

$$Factor = \frac{Std.Conc.}{(\Delta Abs / mn\_Std. - \Delta Abs. / mn\_Blank)}$$

The results will be printed-out:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time: 11:43 am
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method: Concentration Mode v1.00

Sam. 1	Conc.=	0.092 G/L	Abs.= 0.046	Time: 11:43 am
			Abs. 1 = 0.437	
			Abs. 2 = 0.460	
Sam. 2	Conc.=	0.132 G/L	Abs.= 0.066	
			Abs. 1 = 0.447	
			Abs. 2 = 0.480	
Sam. 3	Conc.=	0.220 G/L	Abs.= 0.110	
			Abs. 1 = 0.421	
			Abs. 2 = 0.476	
Sam. 4	Conc.=	0.148 G/L	Abs.= 0.074	
			Abs. 1 = 0.442	
			Abs. 2 = 0.479	

12.2.7 The curve

The deltas of absorbance defined as follows are on the ordinate axis:

$$\Delta Abs./mn\_Sam. - \Delta Abs./mn\_Blank$$

IMPORTANT: For measures with several standards, creation or simulation of calibration curves, measure or simulation of absorbance, saving or not of methods or calibration curves, recall of analyses with stored curves, refer to concentration mode.

Simulation: The values entered by simulation are considered deltas of absorbance and multiplied by the factor. In such case, the absorbance values for the times considered are the last values measured and remain in the display.

12.3 MULTI-WAVELENGTH

12.3.1 Principle

This program allows to make various calculations on a solution measured at several wavelengths (ratio, Allen's correction, ...) and also to know the absorbance value of a solution at different wavelengths (up to 10).

The formula used is of the following type

$$R = \frac{A0 + (A1 \times Abs1) + (A2 \times Abs2) + \dots + (An \times Absn)}{B0 + (B1 \times Abs1) + (B2 \times Abs2) + \dots + (Bn \times Absn)}$$

* R is the result of the calculation.

* $A0, A1, A2, \dots, An, B0, B1, B2, \dots, Bn$ are coefficients which allow for absorbance calculations.

* $Abs1, Abs2, \dots, Absn$ are the absorbances of a solution at $LO1, LO2, \dots, LO_n$

LO being the wavelength.

12.3.2 Calculations

Example: Ratio calculation

(calculation of the purity index of DNA)

The DNA purity index is given by a ratio of the absorbance read at 260 nm by the absorbance read at 280 nm with a trouble deletion by a measurement at 320 nm.

$$R = \frac{Abs_{260nm} - Abs_{320nm}}{Abs_{280nm} - Abs_{320nm}}$$

Here we used 3 wavelengths, then 3 absorbances.

The formula will therefore be:

$$R = \frac{A0 + (A1 \times Abs1) + (A2 \times Abs2) + (A3 \times Abs3)}{B0 + (B1 \times Abs1) + (B2 \times Abs2) + (B3 \times Abs3)}$$

Coefficients $A0, A1, A2, A3, B0, B1, B2, B3$ will be chosen in such a way that the result will be:

If:

$$Abs1 = Abs_{260nm}$$

$$Abs2 = Abs_{280nm}$$

$$Abs3 = Abs_{320nm}$$

The calculation will be:

$$R = \frac{A0 + (A1 \times Abs_{260nm}) + (A2 \times Abs_{280nm}) + (A3 \times Abs_{320nm})}{B0 + (B1 \times Abs_{260nm}) + (B2 \times Abs_{280nm}) + (B3 \times Abs_{320nm})}$$

If:

$$A0 = 0 \quad A1 = 1 \quad A2 = 0 \quad A3 = -1$$

$$B0 = 0 \quad B1 = 0 \quad B2 = 1 \quad B3 = -1$$

We will have:

$$R = \frac{0 + (1 \times Abs_{260nm}) + (0 \times Abs_{280nm}) + ((-1) \times Abs_{320nm})}{0 + (0 \times Abs_{260nm}) + (1 \times Abs_{280nm}) + ((-1) \times Abs_{320nm})}$$

Then

$$R = \frac{Abs_{260nm} - Abs_{320nm}}{Abs_{280nm} - Abs_{320nm}}$$

Other example: Warburg Christian formula for proteins quantification.

$$C_{[Proteins]} = (1,55 \times Abs_{280nm}) - (0,757 \times Abs_{260nm}) \text{ given in mg/mL}$$

Here we used 2 wavelengths, then 2 absorbances.

The calculation is:

$$R = \frac{A0 + (A1 \times Abs1) + (A2 \times Abs2)}{B0 + (B1 \times Abs1) + (B2 \times Abs2)}$$

If:

$$Abs1 = Abs_{280nm}$$

$$Abs2 = Abs_{260nm}$$

The calculation will be:

$$R = \frac{A0 + (A1 \times Abs_{260nm}) + (A2 \times Abs_{280nm})}{B0 + (B1 \times Abs_{260nm}) + (B2 \times Abs_{280nm})}$$

If:

$$A0 = 0 \quad A1 = 1,55 \quad A2 = -0,757$$

$$B0 = 1 \quad B1 = 0 \quad B2 = 0$$

We will have:

$$R = \frac{0 + (1,55 \times Abs_{280nm}) + ((-0,757) \times Abs_{260nm})}{1 + (0 \times Abs_{280nm}) + (1 \times Abs_{260nm})}$$

Then:

$$C_{[Proteines]} = (1,55 \times Abs_{280nm}) - (0,757 \times Abs_{260nm}) \text{ given in mg/mL}$$

Another example : Allen's correction

It allows to make a quantitative measure of a peak in chemical noise.

The formula is:

$$Abs = Abs2 - \frac{(Abs1 + Abs3)}{2} = \frac{2 \times Abs2 - Abs1 - Abs3}{2}$$

For three equidistant wavelengths, the calculation is:

$$R = \frac{A0 + (A1 \times Abs1) + (A2 \times Abs2) + (A3 \times Abs3)}{B0 + (B1 \times Abs1) + (B2 \times Abs2) + (B3 \times Abs3)}$$

If:

$$A0 = 0 \quad A1 = -1 \quad A2 = 2 \quad A3 = -1$$

$$B0 = 2 \quad B1 = 0 \quad B2 = 0 \quad B3 = 0$$

We will then have:

$$R = \frac{0 + ((-1) \times Abs1) + (2 \times Abs2) + ((-1) \times Abs3)}{2 + (0 \times Abs1) + (0 \times Abs2) + (0 \times Abs3)}$$

$$Abs = Abs2 - \frac{(Abs1 + Abs3)}{2} = \frac{2 \times Abs2 - Abs1 - Abs3}{2}$$

12.3.3 Programming the parameters

For the parameters modification, see page 36

Load the method or select "Concentration Mode".

Enter user's name, batch number, samples origin and reagent kit number.

Modify or programme parameters.

Save or not the method.

The general calculation formula in the multiple wavelength mode is displayed at the bottom left of the screen.

* Type of measure

Choose MultiWI

* Reagent blank

YES or NO (See meaning of the blank in this chapter, page 6080)

* Decimal place

from 0 to 3

This parameter defines the number of significant digits after the decimal point.

* Number of standards

Factor

To work with a factor, answer 0.

Choose a value between +/- 10000.

1 standard

To work with 1 standard, answer 1.

Choose a value between 0 and 10000.

Several standards

To work with several standards, enter the number of standards (from 2 through 10).

Choose a value between 0 and 10000.

* Unit

With keyboard, enter the abbreviation wanted.

* X axis (Concentration axis)

Choose between linear and logarithmic

* Y axis (Absorbance axis)

Linear, logarithmic, 1/Abs (1/Y) or Logit. . See Logit axis meaning at the end of this chapter page 80

* Type of curve

Linear (segmented curve), "Regre" (linear regression), "Regre (0)" (linear regression going through the origin 0), Spline. See explanation on the type of curve at the end of this chapter page 81

* Number of wavelengths

From 2 to 10

*** Wavelength**

190 – 900 nm

*** Coeff. Comma**

This parameter defines the number of significant digits after the decimal point for coefficients A0, A1,...,B0, B1,...

*** A0,...,A10**

Choose a value between +/- 10000.

*** B0,...,B10**

Choose a value between +/- 10000.

*** Numbering**

This parameter concerns samples identification.

Auto: Identification of the sample is numerical and increasing.

Example: Sam.1, Sam.2,...

Unit: The user assigns a name to each sample (8 characters) and eventually attributes a dilution factor. See explanation at the end of this chapter, page 88

Table: The user prepares a table in which he will enter the number of samples, their name, and the dilution factor. See explanation at the end of this chapter, page 88

*** Parameters locked**

Allow to locked a method parameters.

YES or NO. See explanation at the end of this chapter, page 90

NOTE: Three parameters (X axis, Y axis, type of curve) can be arbitrarily selected. The user can change them when calibration curve is done. For each parameter changing, the curve will be re drawn by holding account of the new parameter.

12.3.4 Impression of parameters

Press **F2 (Printer)** to print parameters.

12.3.5 Method saving

Press **F3 (Save)** to save method parameters.

12.3.6 Measurement

The procedure for these measurements is the same as for those performed in the concentration mode. The difference will lie in the way of interpreting the readings and the results.

12.3.7 The readings

The absorbances will be measured at different wavelengths as against the blank solution.

12.3.8 The results

They are the results of calculation (ratio, sum) made on absorbances read at different wavelengths.

With the results are displayed the absorbance and transmittance values of the samples

The results will be printed-out:

```

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
Date: Friday november the 21,2003 Time: 11:43 am
User's name: SMITH
Batch number: 123
Origin: HOSPITAL
Kit number: 1256

Method: Concentration Mode v1.00

Sam. 1      Conc.=      0.061      Res.= 0.061      Heure : 14h 59
      W.L. = 266nm      Abs. 1 = 0.240      T% = 57.5
      W.L. = 270nm      Abs. 1 = 0.320      T% = 47.9
      W.L. = 274nm      Abs. 1 = 0.278      T% = 53.7
Sam. 2      Conc.=      0.110      Res.= 0.110
      W.L. = 266nm      Abs. 1 = 0.520      T% = 30.2
      W.L. = 270nm      Abs. 1 = 0.602      T% = 25.0
      W.L. = 274nm      Abs. 1 = 0.499      T% = 31.7
.... ..
    
```

12.3.9 The curve

The results of calculation are displayed on the Y axis.

IMPORTANT: For measures with several standards, creation or simulation of calibration curves, measure or simulation of absorbance, saving or not of methods or calibration curves, recall of analyses with stored curves, refer to the paragraph CONCENTRATION

Simulation: The values entered by simulation are considered as the result of the calculation and are multiplied by the factor.

12.4 DEFINITIONS

12.4.1 Meaning of the blank and calculation

In a number of environments, in particular biological ones, there may be spectral interferences with wavelength of the dosage.

This is the case of colored molecules (haemoglobin, bilirubin, pigments such as carotene, medicines such as methylene blue).

Such interferences which are independent of the parameter to be measured, will be eliminated by measuring the sample alone or with reagent which does not cause any coloring.

It is the **sample blank**.

When there is only one reagent and if the color of the reagent may interfere with the measuring wavelength, it is deducted from the measurement and it is called a **(reagent) blank**.

When there are two reagents, the absorbance of the reagent present in large quantity must be deducted from the blank (mixture of two reagents): it is the **blank of blank**.

NOTE: the terminology of the "blank" is also used for designating the reference solution (water, a component of the reactional mixture,...) which serves for resetting the measurement.

Example :

R1 : Non-triggering reagent.

R2 : Triggering reagent.

Water(XXX) : Quantité d'eau distillée équivalente au produit xxx

Bl.Blank : Abs. of the blank of blank = $R1 + Water(Sam. + R2)$

Blank : Abs. of the (reagent) blank = $R1 + R2 + Water(Sam.)$

Std.Bl : Abs. of the standard blank(s) = $R1 + Std. + Water(R2)$

Std. : Abs. of the standard(s) = $R1 + R2 + Std.$

Sam.Bl. : Abs. of the sample blank(s) = $R1 + Sam. + Water(R2)$

Sam. : Abs. of the sample(s) = $R1 + R2 + Sam.$

The coefficient is given by the following formula:

$$Factor = \frac{Std.Conc.}{(Std. - Std.Bl.) - (Blank - Bl.Blank)}$$

The sample concentration is given by the formula :

$$Sam.Conc = [(Sam.Abs. - Sam.Bl.) - (Blank - Bl.Blank)] Factor$$

12.4.2 Logit axis

The LOGIT is given by the formula

$$L = \frac{\log x}{1 - \log x}$$

With

$$X = \frac{B}{B0}$$

B = Sample absorbance – Reagent blank absorbance.

$B0$ = Zero standard absorbance - Reagent blank absorbance.

IMPORTANT: If the event of a calibration with a LOGIT axis (Ex: Immuno-enzymology), it is necessary to program a zero standard with no concentration but with an absorbance higher than that of all the standards.

12.4.3 Explanation of the various types of curve

Straight line

The calibration line consists of segments of straight line which link the calibration points together.

Spline

To be used mainly for a non-linear calibration.

It is the curve defined by the juxtaposition of several 3rd-degree curves which meet between each point, and the 1st and 2nd derivatives of which also meet.

To calculate all the coefficients of the 3rd-degree curves, the algorithm moves along a sequence of approximations with the following criteria:

- The curves must cross a rectangle of uncertainty centered on the measuring point.
- The number of points of inflexion must be as small as possible.
- The area between the square of the second derivative curve and the X axis must be as small as possible.
- After 4 or 5 iterations, the coefficients converge towards the coefficients specific of the curve searched for.

Advantages of the spline function

This curve does not necessarily run through all the measuring points; therefore if a point drifts away from the theoretical curve, the algorithm will not cause the curve to go through such point and the calculations will be closer to reality.

The very definition of the spline function which tends to bring the model of the curve closer to that of a straight line, deletes all "undulated curves". The curve will be closer to the theoretical curves which are regular.

This type of function must be used in between extreme values. No extrapolation is to be made.

Regression (noted "Regre")

To be used mainly when the theoretical curve must be a straight line.

It is a straight line which goes through the calibration points where the square of distances between such points and the straight line vertically, has been minimized.

Regression passing by the origin [noted "Regre (0)"]

To be used mainly when the theoretical curve must be a straight line and have to go through the origin.

It is a straight line calculated by the smallest rectangle mode.

It is a straight line which goes through the calibration points where the square of distances between such points and the straight line, diagonally, has been minimized and pass by the origin.

12.5 PARTICULAR WORKINGS

12.5.1 Simulation

It is possible to simulate readings which is very helpful for programs with calibration curves.

When the user has forgotten to save the calibration, can rebuilt it if he knows the concentrations and the absorbances of the standards.

Press **F2 (Simulation)**.

Enter the absorbances values (blank, standards, samples) ranging from -1,000 and +3,000 with the keyboard.

The display and the printing of the results will be made as a true measurement.

Example of a calibration curve:

Enter in the concentration mode. Look for the following screen

```

F1-Measure  F2-Simulation  F3-Parameters  Esc-Quit
2008/12/10 15:53:12

Concentration Mode v1.00

CELL A Blank
CELL B Std. 1
CELL C Std. 2
CELL D Std. 3
CELL E Std. 4

RESULTS
Conc.      Abs.

Sample

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```

Press **F2 (Simulation)** to built the calibration curve.

```

Abs. Cell A = 0.020
2009/12/10 15:54:45
Concentration Mode v1.00
RESULTS
Sample Conc. Abs.
CELL A Blank
CELL B Std. 1
CELL C Std. 2
CELL D Std. 3
CELL E Std. 4
Esc ABCDEFGHIJKLMNOPQRSTUVWXYZ Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % ( ) _ : ; " ' , . ~ Enter
Copyright SECOMAM SIMULATION

```

Enter the different absorbance values of the blank and the standards.

They will be printed and displayed as true measurements.

The operator will eventually continue with samples absorbance.

12.5.2 Calibration anomalies

During the calibration curve setting up, it is possible that different anomaly messages are displayed.

F1-X axis	F2-Y axis	F3-Type	F4-New Calibration	2003/12/10 16:04:46
-----------	-----------	---------	--------------------	---------------------

Concentration Mode v1.00

CELL		RESULTS		
	CELL	Sample	Conc.	Abs.
CELL A	Blank	Blank		0.020
CELL B	Std.	Std. 1	10.0 g/l	0.185
CELL C	Std.	Std. 2	20.0 g/l	0.370
CELL D	Std.	Std. 3	30.0 g/l	0.270
CELL E	Std.	Std. 4	40.0 g/l	0.581

It is necessary to verify if:

- The concentration values entered in the parameters are monotonous.
- The absorbance values of the standards are monotonous.
- The standards were measured in the correct order.
- The absorbance of the standard at a zero concentration is higher than that of all the standards (as is the case with a LOGIT absorbance axis).

- The absorbance of the first standard is not nil (as is the case with a logarithmic absorbance axis).
- The concentration of the first standard is not nil (as the case with a logarithmic concentration axis).

The operator may:

- Change either of both axis if they were poorly selected.
- Change, if need be, the concentration of the standards in the parameters window.
- Recalibrate by entering **F4 (New calibration)**.

12.5.3 Saving the analysis

If the user has entered a factor, a standard or several standards, the analysis saving is the same.

When parameters are entered, it displays:

F1-Modification F2-Printer F3-Save Esc-Quit 2003/12/10 16:31:37

Concentration Mode v1.00

PARAMETERS

Type of measure : Abs

Wavelength (nm):	500	
Reagent blank :	Yes	
Sample blank :	No	
Decimal place (0-3):	1	
No of standards (0-10):	4	
Conc. 1 (0-10000) :	10.0	
Conc. 2 (0-10000) :	20.0	
Conc. 3 (0-10000) :	30.0	
Conc. 4 (0-10000) :	40.0	
Unit :	g/l	
X axis (Concentration):	Lin	
Y axis (Absorbance):	Lin	
Type of curve :	Linear	

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Press **F3 (Save)**.

File name (8 Characters) : CONCENTR 2003/12/10 16:33:15

Concentration Mode v1.00

PARAMETERS

Type of measure : Abs

Wavelength (nm):	500	
Reagent blank :	Yes	
Sample blank :	No	
Decimal place (0-3):	1	
No of standards (0-10):	4	
Conc. 1 (0-10000) :	10.0	
Conc. 2 (0-10000) :	20.0	
Conc. 3 (0-10000) :	30.0	
Conc. 4 (0-10000) :	40.0	
Unit :	g/l	
X axis (Concentration):	Lin	
Y axis (Absorbance):	Lin	
Type of curve :	Linear	

Esc ABCDEFGHIJKLMNOPQRSTUVWXYZ Back
 Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () _ { } | ~ `

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Enter, using 8 capital letters the file name. Confirm.

Title name (30 Characters) : CONCENTRATION WITH 4 STANDARDS 2003/12/10 16:35:47

Concentration Mode v1.00

PARAMETERS

Type of measure : Abs

Wavelength (nm):	500	
Reagent blank :	Yes	
Sample blank :	No	
Decimal place (0-3):	1	
No of standards (0-10):	4	
Conc. 1 (0-10000) :	10.0	
Conc. 2 (0-10000) :	20.0	
Conc. 3 (0-10000) :	30.0	
Conc. 4 (0-10000) :	40.0	
Unit :	g/l	
X axis (Concentration):	Lin	
Y axis (Absorbance):	Lin	
Type of curve :	Linear	

Esc ABCDEFGHIJKLMNOPQRSTUVWXYZ Back
 Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () _ { } | ~ `

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Enter the full name of the method (up to 30 characters). This information will appear in the top side of the window in place of CALCULATION MODE. Confirm.

F1-Execute F2-Parameters F3-File results Esc-Quit 2003/12/10 16:38:35

CONCENTRATION WITH 4 STANDARDS v1.00

PARAMETERS

Type of measure	:	Abs
Wavelength (nm):	:	500
Reagent blank	:	Yes
Sample blank	:	No
Decimal place (0-3):	:	1
No of standards (0-10):	:	4
Conc. 1 (0-10000):	:	10.0
Conc. 2 (0-10000):	:	20.0
Conc. 3 (0-10000):	:	30.0
Conc. 4 (0-10000):	:	40.0
Unit	:	g/l
X axis (Concentration):	:	Lin
Y axis (Absorbance):	:	Lin
Type of curve	:	Linear

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The file name and method name will appear in the main menu.

F1-Config F2-Editor file F3-Tools F4-Choice F5-Selection 2003/12/10 16:40:55

SECOMAM - Uvi Light v1.00 SIMULATION

Program choices

Absorbance Mode	v1.00	04/11/2003
Kinetic mode	v1.00	04/11/2003
Concentration Mode	v1.00	04/11/2003
CONCENTRATION WITH 4 STANDARDS CONCENTR	v1.00	10/12/2003
Spectrum Mode	v1.00	04/11/2003

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If the user does not want to save the analysis, he will enter **ESC** in place of **F3 (Save)**.

Parameters have not been saved, continue (Yes [ENT]/No [ESC])? 2003/12/10 16:46:12

CONCENTRATION WITH 4 STANDARDS v1.00

PARAMETERS

Type of measure	:	Abs
Sample blank	:	No
Decimal place (0-3):	:	1
No of standards (0-10):	:	4
Conc. 1 (0-10000):	:	10.0
Conc. 2 (0-10000):	:	20.0
Conc. 3 (0-10000):	:	30.0
Conc. 4 (0-10000):	:	40.0
Unit	:	g/l
X axis (Concentration):	:	Lin
Y axis (Absorbance):	:	Lin
Type of curve	:	Linear
Numbering	:	Auto
Parameters locked	:	No

Esc ABCDEFGHIJKLMNOPQRSTUVWXYZ Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % () ^ _ Enter

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Press **ENT** to continue the measuring process. Press **ESC** to return to the previous screen.

12.5.4 Recalling of a stored analysis

12.5.4.1 Analysis using a factor

Load the method

Enter the parameters for the traceability.

F1-Execute		F2-Parameters		F3-File results		Esc-Quit		2003/12/10 16:53:28	
CONCENTRATION WITH 4 STANDARDS v1.00									
PARAMETERS									
Type of measure		:	Abs						
Wavelength (nm):		:	500						
Reagent blank		:	Yes						
Sample blank		:	No						
Decimal place (0-3):		:	1						
No of standards (0-10):		:	0						
Factor (+/-10000):		:	100.0						
Unit		:	G/L						
Numbering		:	Auto						
Parameters locked		:	No						
Copyright SECAM SIMULATION									

Press **F1 (Execute)** to start the analysis.

12.5.4.2 Analysis using one standard

Load the method.

Enter parameters for the traceability.

Press **F1 (execute)**.

If the standard value has been saved with the method, it displays:

F1-Keep Standards		F2-Redo 1 Std.		2003/12/10 17:00:28	
CONCENTRATION WITH 1 STANDARD v1.00					
PARAMETERS					
Type of measure		:	Abs		
Wavelength (nm):		:	500		
Reagent blank		:	Yes		
Sample blank		:	No		
Decimal place (0-3):		:	1		
No of standards (0-10):		:	1		
Concentration(0-10000):		:	2.5		
Unit		:	G/L		
Numbering		:	Auto		
Parameters locked		:	No		
RESULTS					
Sample		Conc.		Abs.	
Copyright SECAM SIMULATION					

- No new measure. Enter **F1 (Keep Standards)**.

The sample measurements will be done using the standard value previously read.

- New measure of the whole. Enter **F2 (Redo 1 Std.)**.

Measure the standard before measuring the samples.

"Delete the previous calibration (Yes [ENT]/No [ESC])?"

NO: It keeps in memory the previous value of the standard, but it works with the new standard value for this sample batch.

YES: The new standard value is saved in memory.

12.5.4.3 Analysis using several standards

Load the method.

Enter the parameters for the traceability.

Press **F1 (Execute)**.

If the calibration curve has been saved with the method, it will display:

F1-Keep Standards		F2-Redo 1 Std.		F3-Redo All Std.		2008/12/10 17:16:46	
CONCENTRATION WITH 4 STANDARDS v1.00							
PARAMETERS				RESULTS			
Type of measure :		Abs		Sample		Conc. Abs.	
Wavelength (nm):		500					
Reagent blank :		Yes					
Sample blank :		No					
Decimal place (0-3):		1					
No of standards (0-10):		4					
Conc. 1 (0-10000):		10.0					
Conc. 2 (0-10000):		20.0					
Conc. 3 (0-10000):		30.0					
Conc. 4 (0-10000):		40.0					
Unit :		g/l					
X axis (Concentration):		Lin					
Y axis (Absorbance):		Lin					
Type of curve :		Linear					
Copyright SECAM SIMULATION							

It is possible to retrieve it, to work with the curve, to recalibrate it or to draw a new one.

- No new measure. Enter **F1 (Keep Standards)**.

The curve which was stored is then displayed. It is ready for measurement.

- New measure of the whole. Enter **F2 (Redo 1 Std.)**.

Enter the number of the standard to be re-read. Confirm.

Prepare the multicell holder as indicated.

Press F1 (Measure) to start the measurement.

- It will consider that all the standards in the range have evolved similarly and will recalculate the absorbance of each of them.

NOTE: The recalibration process consists in shifting the curve in view of the new blank (if any) and in performing an homothetic transformation which allows to juxtapose the former value of the standard with the new one.

"Delete the previous calibration (Yes [ENT]/No [ESC])?"

NO: It keeps in memory the previous calibration curve, but it works with the new calibration curve for this sample batch.

YES: The new calibration curve is saved in memory.

- New measure of the whole. Enter **F2 (Redo All Std.)**.

Measure again the blank (if any) and the standards.

12.5.5 Files results

Uvi Light offers the possibility to keep the results of the analysis in the form of ASCII files. Such files may be retrieved by copying them on floppy disk to run them on other computer systems (Excel,...)

F1-Execute		F2-Parameters		F3-File results		Esc-Quit		2008/12/11 07:39:44	
CONCENTRATION WITH 4 STANDARDS v1.00									
PARAMETERS									
Type of measure :		Abs							
Sample blank :		No							
Decimal place (0-3):		1							
No of standards (0-10):		4							
Conc. 1 (0-10000):		10.0							
Conc. 2 (0-10000):		20.0							
Conc. 3 (0-10000):		30.0							
Conc. 4 (0-10000):		40.0							
Unit :		g/l							
X axis (Concentration):		Lin							
Y axis (Absorbance):		Lin							
Type of curve :		Regre							
Numbering :		Auto							
Parameters locked :		No							
Copyright SECAM SIMULATION									

Press F3 (File results). It displays:

-87-

Entrer number of cell (1-8): 2003/12/11 08:11:34

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A Reference			
CELL B Std.			
CELL C Sam.	1		
CELL D Sam.	2		
CELL E Sam.	3		
CELL F Sam.	4		
CELL G Sam.	5		
CELL H Sam.	6		
CELL I Sam.	7		
Std. Factor =	57.9	10.0 g/l	0.173
Sam.	1	22.1 g/l	0.381
Sam.	2	35.3 g/l	0.610
Sam.	3	42.8 g/l	0.739
Sam.	4	57.3 g/l	0.989
Sam.	5	59.0 g/l	1.019
Sam.	6	62.0 g/l	1.192
Sam.	7	87.7 g/l	1.514

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12.5.6.2 Unit identification

Select "Unit" for the "Numbering" parameter.

Charge factor

It is possible for certain reagents (VWR,...) to enter a factor (F) which is a correction factor corresponding to the reagent batch used.

The factor ranges between 0.9 and 1.1 and is initialized to 1.

The value of the results is multiplied by such factor.

If the operator does not want to change it, he just has to confirm it; otherwise he will enter the new value and confirm.

Dilution factor

The dilution factor ranges from 1 to 999 and is initialized at 1.

The value of the results is multiplied by such factor.

When the operator has confirmed the sample name, the cursor positions itself on the dilution factor.

If the operator does not want to change it, he will just have to confirm it; otherwise, he will enter the new value and confirm.

Name of Sam. 9 : KIT123F 2003/12/11 08:31:30

Concentration Mode v1.00

CELL		RESULTS	
Sample	Conc.	Abs.	
CELL A Reference			
CELL B KIT123E			
Std. Factor =	49.1	10.0 g/l	0.204
ASSAY01	20.4 g/l	0.416	
ASSAY02	26.1 g/l	0.532	
ASSAY03	34.3 g/l	0.699	
ASSAY04	40.9 g/l	0.833	
ASSAY05	54.2 g/l	1.104	
ASSAY06	64.8 g/l	1.320	
ASSAY07	76.4 g/l	1.556	

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The operator assigns a name (8characters) and, if need be, a dilution factor to the sample.

12.5.6.3 Identification using a table

Select "Table" for the "Numbering" parameter.

Enter or not the charge factor (see precedent paragraph).

The user prepares a table with measuring samples number, their name and eventually a dilution factor.

Press F1 (Execute).

+↑↓→	Move	F5-Name	F6-Dilution	F7-Sample (Nb)	F8-Print	F9-End	2003/12/11 08:51:19
->	1	Sam. 1	x	1.0	<-		
	2	Sam. 2	x	1.0			
	3	Sam. 3	x	1.0			
	4	Sam. 4	x	1.0			
	5	Sam. 5	x	1.0			
	6	Sam. 6	x	1.0			
	7	Sam. 7	x	1.0			
	8	Sam. 8	x	1.0			
	9	Sam. 9	x	1.0			
	10	Sam. 10	x	1.0			

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- Dimension the table by entering **F7 [Sample (Nb)]**.
- Enter the number of samples (from 1 to 120).
- Place the cursor on the sample to be identified by means of the direction arrows.
- Enter **F5 (Name)** and then the 8-characters name. Confirm.
- Enter **F6 (Dilution)** and then the dilution factor (from 1 to 999).

The dilution factors are initially 1.

Example:

+↑↓→	Move	F5-Name	F6-Dilution	F7-Sample (Nb)	F8-Print	F9-End	2003/12/11 09:05:38
	1	KIT123A	x	2.0			
	2	KIT123B	x	1.0			
	3	KIT123C	x	4.0			
	4	KIT123D	x	3.0			
	5	KIT123E	x	2.0			
	6	KIT123F	x	2.0			
	7	KIT123G	x	1.0			
->	8	KIT123H	x	3.0	<-		

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Press **F8 (Print)**.

The results will be printed-out:

```

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi
Light v1.00
Date: Friday november the 21,2003 Time: 11:43 am
User's name: SMITH
Batch number: 123
Origin: HOSPITAL
Kit number: 1256

Method: Concentration Mode v1.00

Table of sample names

1 KIT123A      x  2.0
2 KIT123B      x  1.0
3 KIT123C      x  4.0
4 KIT123D      x  3.0
5 KIT123E      x  2.0
6 KIT123F      x  2.0
7 KIT123G      x  1.0
8 KIT123H      x  3.0
    
```

Once the table is ready, enter **F9 (End)**.

F1-Measure F2-Simulation F3-Parameters Esc-Quit 2003/12/11 09:18:05

Concentration Mode v1.00

Sample	RESULTS Conc.	Abs.
CELL A Reference		
CELL B Std.		
CELL C KIT123A		
CELL D KIT123B		
CELL E KIT123C		
CELL F KIT123D		
CELL G KIT123E		
CELL H KIT123F		
CELL I KIT123G		

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launch the measurement by entering **F1 (Measure)**.

F1-Other Table F2-Remeasure Table Esc-Quit 2003/12/11 09:23:17

Concentration Mode v1.00

Sample	RESULTS Conc.	Abs.
CELL A Reference		
CELL B KIT123H		
Std. Factor =	10.0 g/l	0.142
KIT123A	44.4 g/l	0.315
KIT123B	39.6 g/l	0.561
KIT123C	215.6 g/l	0.764
KIT123D	184.3 g/l	0.871
KIT123E	153.9 g/l	1.090
KIT123F	164.6 g/l	1.166
KIT123G	112.3 g/l	1.591
KIT123H	38.7 g/l	0.183

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To measure the table again with the same configuration, enter **F2 (Remeasure table)**.

To prepare another table, enter **F1 (Other table)**.

12.5.7 Locked parameters

Allow to lock the analysis parameters.

Select **"Yes"** for **"Parameters locked"** in the parameters window.

If the operator wants to modify a locked analysis, the following message will appear:

Parameters locked ... ANALYSIS LOCKED v1.00 2003/12/11 09:34:55

PARAMETERS	
Type of measure	Abs
Wavelength (nm):	500
Reagent blank :	No
Sample blank :	No
Decimal place (0-3):	1
No of standards (0-10):	1
Concentration(0-10000):	10.0
Unit :	g/l
Numbering :	Auto
Parameters locked :	Yes

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It is not possible to unlock an analysis. You have delete it (see page 94) and create a new one.

13 SPECTRUM MODE

The spectrum mode is used for measuring the absorbance or transmission of a sample by reference to the wavelength. It is especially useful to look for peaks of absorption in solutions and, more generally speaking, to know the behavior of a solution at different wavelengths.

The spectrum mode also offers the opportunity to process curves which have already been saved or acquired by the operator.

Load the method or select "Spectrum Mode". Confirm.

Introduction of datas
2003/12/02 16:53:54

User's name
Batch number
Origin
Kit number

:
:
:
:

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % _ () µ ± . . . Enter

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SIMULATION

Enter:

- The user's name (20characters: signs, letters, numbers).
- The batch number (8 characters: signs, letters, numbers).
- The origin (30 characters: signs, letters, numbers).
- Kit number (8 characters: signs, letters, numbers).

These information are necessary for measurement traceability (ISO 9000, G.L.P,...) and will be printed with the results.

Press ESC to skip this step.

13.1 PROGRAMMING THE PARAMETERS

For the parameters modification, see page 36

F1-Modification	F2-Printer	F3-Save	Esc-Return	2003/12/02 16:56:34
-----------------	------------	---------	------------	---------------------

Spectrum Mode v1.00

<table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th colspan="2" style="text-align: left;">PARAMETERS</th> </tr> </thead> <tbody> <tr> <td>wavelength 2 (nm):</td> <td style="text-align: right;">900</td> </tr> <tr> <td>wavelength 1 (nm):</td> <td style="text-align: right;">190</td> </tr> <tr> <td>wavelength chan. (320-375):</td> <td style="text-align: right;">330</td> </tr> <tr> <td>Speed (100-2400):</td> <td style="text-align: right;">1800</td> </tr> <tr> <td>Y axis :</td> <td style="text-align: right;">Absorb.</td> </tr> <tr> <td>Parameters locked :</td> <td style="text-align: right;">No</td> </tr> </tbody> </table>	PARAMETERS		wavelength 2 (nm):	900	wavelength 1 (nm):	190	wavelength chan. (320-375):	330	Speed (100-2400):	1800	Y axis :	Absorb.	Parameters locked :	No	<table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left;">RESULTS</th> </tr> </thead> <tbody> <!-- Empty table body --> </tbody> </table>	RESULTS
PARAMETERS																
wavelength 2 (nm):	900															
wavelength 1 (nm):	190															
wavelength chan. (320-375):	330															
Speed (100-2400):	1800															
Y axis :	Absorb.															
Parameters locked :	No															
RESULTS																

Copyright SECOMAM SIMULATION

Press **F2 (Parameters)**, then F1 (Modification).

*** Wavelength 2**

Final wavelength of the scan. Choose between 190 and 900 nm.

*** Wavelength 1**

Initial wavelength of the spectrum. Choose between 190 and 900 nm.

*** Wavelength change (320-375)**

To prevent any switching from the deuterium lamp to the halogen and vice versa on an interesting peak of the spectrum, the operator may shift the switching point.

Choose any value between 320 and 375 nm.

*** Speed (100-2400)**

This is the average speed of wavelengths at small absorbances, expressed in nanometers per minute. Continuous variation between 100 and 2400 nm/mn. The step is 1 nm.

N.B. 9.2: The smaller the speed, the greater the number of elementary measurements and since the background noise is inversely proportional to the square root of the number of measurements, it will be even smaller.

*** Type of axis**

The operator may choose between Absorbance and Transmittance for the Y axis.

*** Parameters locked**

Allow to lock the analysis parameters. See page 90

At the end of the modification of parameters, confirm.

13.2 PRINTING THE PARAMETERS

Press **F2 (Printer)** for printing out the parameters.

13.3 SAVING THE METHOD

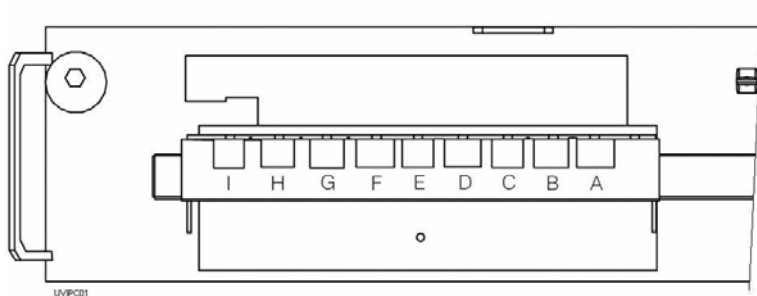
Press **F3 (Save)** to save parameters.

13.4 MEASUREMENT

Prepare the multi-cell holder as follows:

Position A:	Blank (reagent) or reference.
Position B through I:	Samples.

Through the measuring sequence, the multi-cell holder will be prepared in the same way.



Introduction of datas
2003/12/02 17:12:10

Spectrum Mode v1.00

PARAMETERS		RESULTS
Wavelength 2 (nm):	400	
Wavelength 1 (nm):	190	
Wavelength chan. (320-375):	330	
Speed (100-2400):	1800	
Y axis:	Absorb.	
Parameters locked:	No	

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % _ () µ ± Enter
Copyright SECOMAM SIMULATION

Press **F1 (Measure)** to start the measure.

Enter the number of samples to be measured.

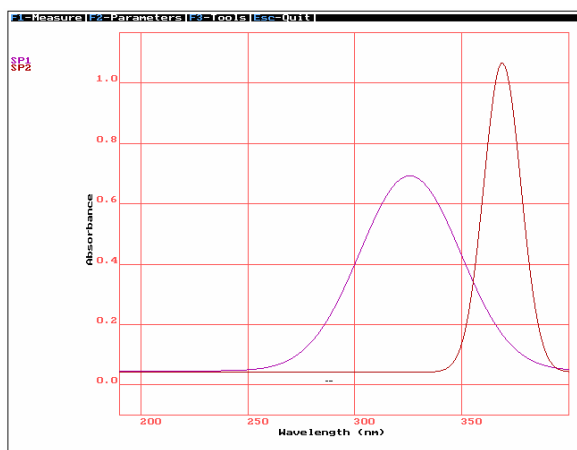
Confirm

After reading the basic line on the cell in "A" position, the spectrophotometer will make the acquisition of the scans one by one, starting with the cell on B position.

It displays one by one every scan progressively with their acquisition

The scan will be saved temporarily under the form SP (Index)

The name with the higher index will be the last scan performed by operator.



13.5 TOOLS

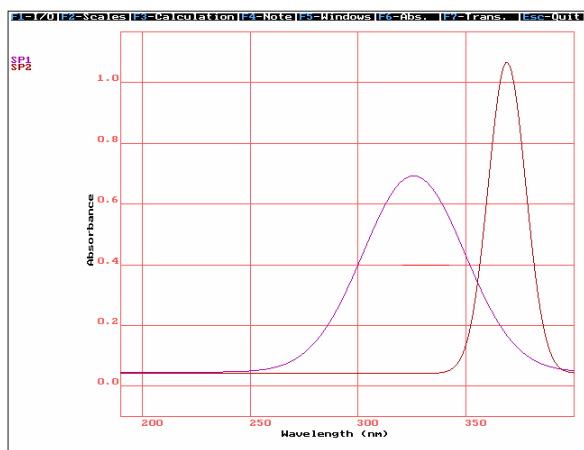
Press **F3 (Tools)**.

This sub-routine is used for various processings (zoom, derivative,...) or calculation on the curves stored in memory.

13.5.1 Input/output

This function allows to load, save, delete, print one or several curves.

Press **F1 (I/O)**.



13.5.1.1 Save

The curves may be saved one by one or several all together with some comments (what is called image).

NOTE: The images are different from curves and it is not possible to superimpose between them or with curves.

a) Curves saving

Maximum curve saving capacity on hard disk: 1500 spectra. It is possible to increase the memory storage capacity by using the "Save" routine which allows to export or import curves on a diskette. See page 80

Press **F2 (Save)**, then **F1 (Curve)**.

No curve must be saved, return to the previous menu. Otherwise choose the curve(s) to be stored among the curves drawn. Confirm. Enter the name in 8 digits, confirm. Return to the previous menu.

b) Images saving

Maximum image saving capacity on hard disk: 1500 images.

Press **F2 (Save)**, then **F2 (Image)**.

Enter the name in 8 digits, confirm.

NOTE: It is advised to write as a comment, the image file name

13.5.1.2 Load

This function is used for loading one or several spectra (up to 9) on the screen, for various processing (zoom) or calculation (derivatives, operations, peak read-outs,...)

NOTE: Upon the first entry in the spectra analysis mode and after loading the tools function **F3 (Tools)**, the display strip shows **F1 (I/O)**, **F2 (Calculation)** **Esc (Quit)**.

If spectra have been saved, it is possible to load one of several of them. If there is no spectrum in the memory, the functions **Load** and **calculation** loop back.

Return to the previous menu with the **Esc** key.

a) Curves loading

Press **F1 (Load)**, **F1 (Curve)**.

In the spectrum library proposed, the spectra saved (Example: DERIVATIVE – DIDYME – HOLMIUM) and the spectra recently performed (SPxx) are of different colors.

The later will be deleted as soon as the spectra mode is closed. Choose the spectrum or spectra to be loaded, confirm and confirm.

b) Images loading

Press **F1 (Load)**, **F2 (Image)**.

In the image library proposed, choose the one to recall, confirm and confirm.

13.5.1.3 Delete

This function allows to delete one or several curves chosen by the user.

Press **F3 (Delete)**.

Choose the curve(s) to be deleted, confirm and confirm.

The curve(s) will be deleted.

13.5.1.4 Print

Press **F4 (Print)**.

The curve(s) will be printed horizontally without comments in a 11x21 cm format.

13.5.1.5 Hardcopy

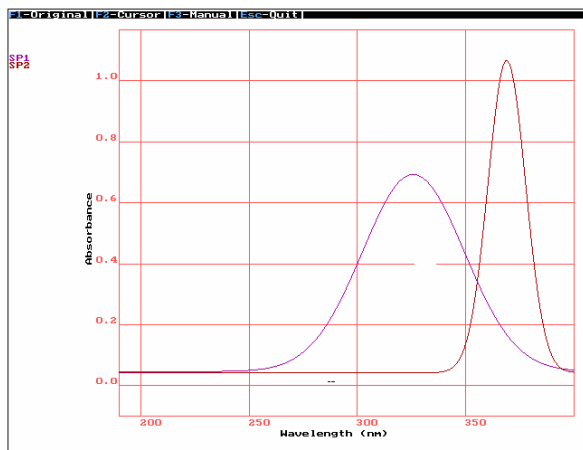
Press **F5 (Hardcopy)**.

The curve(s) will be printed vertically with comments in a 21x29.7 cm format.

13.5.2 Scales

This function allows to expand an interesting section of a curve.

-Press **F2 (Scales)**.



NOTE: Throughout the function, the **Esc** key allows to return to the previous menu.

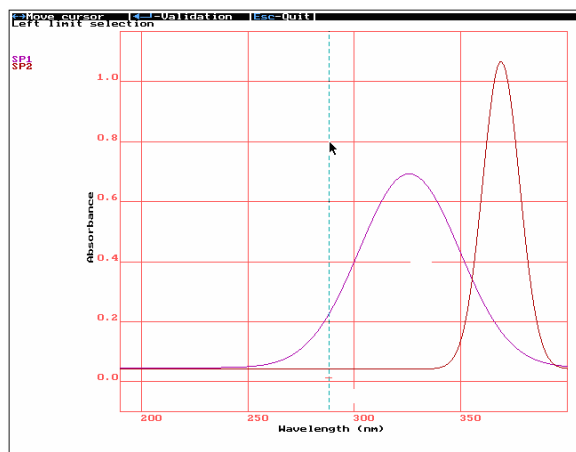
13.5.3 Original

This command allows to return to the initial curve after a manual or with mouse expansion

Press **F1 (Original)**.

13.5.3.1 Zoom with cursor

-Press **F2 (Cursor)**.

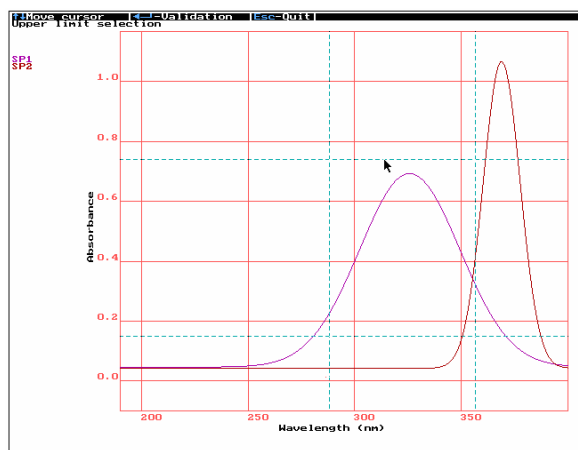


Select the left limit of the section to be expanded by moving the cursors with the ← and → keys. Confirm.

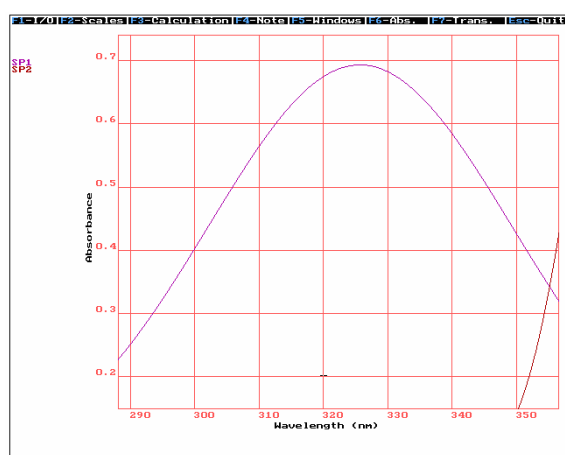
Similarly select the right limit of the section to be expanded. Confirm

Frame at the top and the bottom the section to be expanded by moving the cursor with the ↑ and ↓ keys and validating whenever it reaches the correct position.

Example:



Confirm.



To retrieve the initial curve, enter **F2 (Scales)**, then **F1 (Original)**.

13.5.3.2 Manual zoom

Press **F3 (Manual)**.

Enter the wavelength scales.

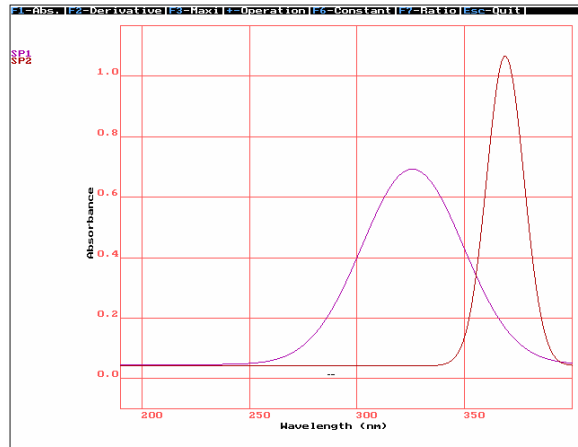
Automatic zoom?

YES: The unit recalculates the absorbance scales automatically.

NO: Enter the absorbance scales.

13.5.4 Calculation

Press **F3 (Calculation)**.



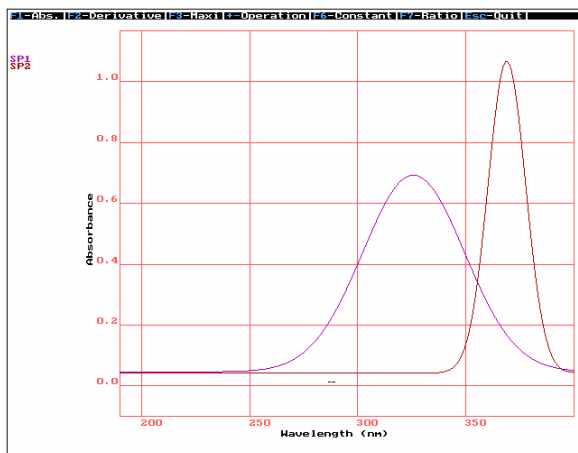
This function allows to:

- read the absorbance on one or several spectra at a given wavelength.
- calculate the derivatives
- determine the peaks or valleys on one or several spectra.
- add two spectra
- subtract one spectrum from another.
- multiply a spectrum by a coefficient.
- add a constant to a spectrum.
- perform a ratio calculation between two absorbances at different wavelengths.

13.5.4.1 Absorbance

Allows to read an absorbance in view of wavelength on one or several spectra.

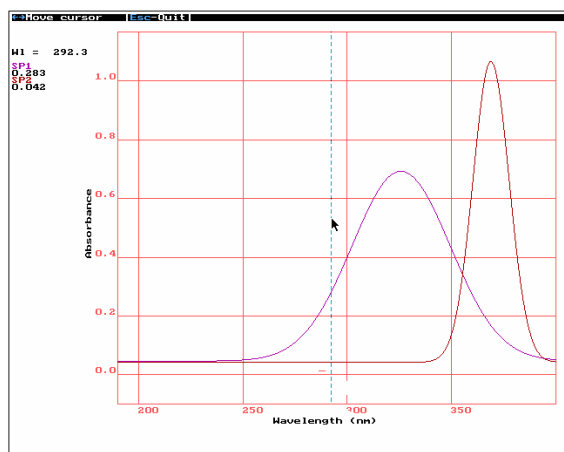
-Press **F1 (Abs.)**.



a) With cursor

The absorbance of the one or several curves can be read simultaneously depending on the position of a cursor moved by the operator.

Press **F1 (Cursor)**.



At the top left of the screen the wavelength in nanometers with the name of each curve and absorbance corresponding to such wavelength below are displayed. It is possible to change the position of the cursor by means of the ← and → keys. With each new position of the cursor, new Wavelength/Absorbance couples are displayed.

b) Manual

Press **F2 (Manual)**.

Enter wavelength in nanometers. ANTHELIE Data will display the absorbance value for the curve(s) visualized on the monitor.

For both modes (with cursor and manual), the command **F4 (Hardcopy)** allows to print the curve(s) with the values. The command **F3 (Print)** only prints out the values.

L.O. = 220.1	Time: 1:50 pm
SP1 Abs.= 0.349	T% = 44.8
SP2 Abs.= 0.932	T% = 11.7

The command **ESC** allows to return to the previous menu.

13.5.4.2 Derivatives

It is possible to derive a spectrum up to 4th order. It allows to eliminate a linear or non linear noise, to look for the absorption peaks of solutions in a mixture, etc.

NOTE: The derivative of zero order allows to smooth out the curve.

* CALCULATION OF DERIVATIVES

A window the width of which corresponds to the differentiation step (in nanometers) is moved over the spectrum; the difference between two windows is defined by the measuring step.

Within each window, a mean slope is calculated.

The value of the slope is entered in the center of the window and point of the derivative curve is thus obtained.

* METHOD OF CALCULATION

A method derived from the Stavitzky-Golay method is used for obtaining the derivative spectrum; a fraction of the curve contained in the calculation window is defined by an equation of the following type:

$$y = a_3 x^3 + a_2 x^2 + a_1 x + a_0$$

From the central point of the window, coefficients are calculated with the least square method.

The coefficients help to take into account the distance of the point to the center of the window and to calculate a weighted average along the following formula:

$$Y_j = \frac{\sum_{i=-m}^{i=m} C_i Y_{j+i}}{N_s n}$$

C_i = Weighting coefficient

Y_j = Absorbance

$N_s n$ = Normalization factor

This method allows to smooth and derive the curves by simply making a weighted average.

The signal/noise ratio can therefore increase significantly (just increase the number of points and therefore expand the calculation window). However the spectrum may be distorted owing to the width of the window.

Actually the value of the derivative decreases when the calculation window is expanded. It also depends on the order of derivative: the higher the order, the greater the reduction).

Press **F2 (Derivative)**.

Choose the spectrum to be derived.

Choose the order of the derivative and the differentiative step.

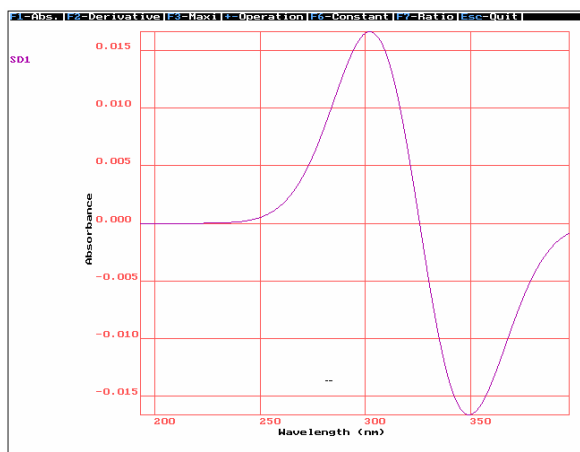
The step expressed in nm corresponds to the width of the smoothing window.

Example:

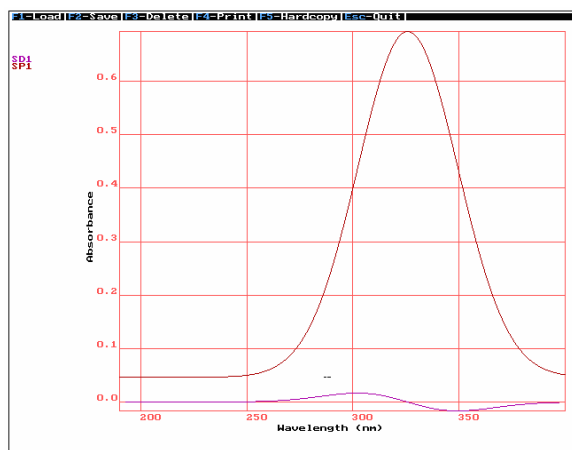
Spectrum: SP1

Order: 1

Step: 5 nm



The derived curve is saved temporarily under the name SD (index) and may be retrieved for superposition with the initial spectrum.



13.5.4.3 Maxi

This function allows to read automatically the absorbance value of the peaks or valleys of the spectrum/spectra loaded on the monitor.

Press **F3 (maxi)**.

a) Peaks

Press **F1 (Peaks)**.

Choose the gap. Example = 0.1A.

Gap: Absorbance value which will define a peak detection threshold. Only the peaks the height of which (difference between the top and nearest valley) is higher than the absorbance value (gap) will be displayed and printed.

F1-Printer		Esc-Quit		2003/12/05 14:23:48	
PARAMETERS		SCANNING MODE		v1.00	
Wavelength 2	(nm):	400			
Wavelength 1	(nm):	190			
Wavelength chan. (320-375):		330			
Speed	(100-2400):	1800			
Y axis	:	Absorb.			
Parameters locked	:	No			
		RESULTS			
		Peaks of SP1			
		325.7 Abs = 0.693			
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It is possible to print the results by entering **F1 (Printer)**. Press **ESC** twice and enter **F4 (Graphic)** to return to the curve.

b) Valleys

-Press **F2 (Valleys)**.

Choose the gap. Example:0.2A.

Gap: absorbance value which define a peak detection threshold. Only the valleys the depth of which (difference in terms of absorbance between the bottom and nearest peak) will be printed and displayed.

It is possible to print the results by entering P(Printer). Press **ESC** twice and enter G (Graphic) to return to the curve.

It is possible to print the results by entering **F1 (Printer)**. Press **ESC** twice and enter **F4 (Graphic)** to return to the curve.

13.5.4.4 Addition

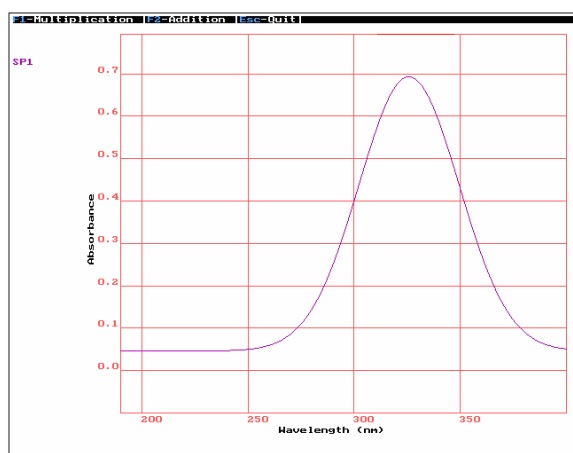
Allows to add two curves. Enter **+** (**+ Operation**). Choose the first curve, confirm. Choose the second curve, confirm. The new curve is displayed and temporarily stored under the name **SA (index)**.

13.5.4.5 Substraction

Allows to subtract one curve from another. Enter **-** (**+Operation**). Choose the first curve, confirm. Choose the second curve, confirm. The new curve is displayed and temporarily stored under the name **SA (index)**.

13.5.4.6 Constant

Press **F6 (Constant)**.



a) * Multiplication

Allows to multiply a curve by a positive or negative number.

Enter* (**multiplication**). Choose the curve. Enter the multiplying coefficient and confirm. The new curve is displayed and stored temporarily under the name **SM (index)**.

b) + Addition

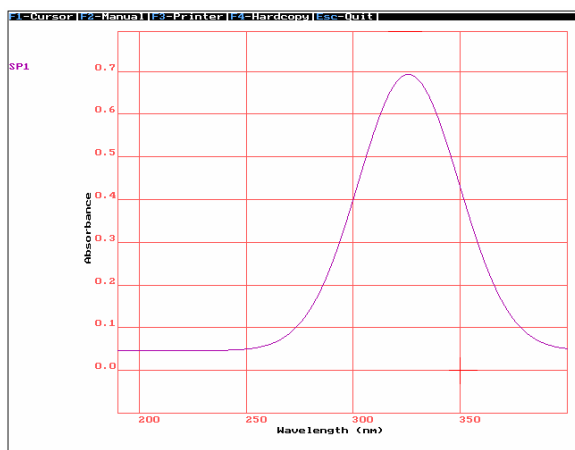
Allows to add positive or negative constant to the curve to shift it upwards or downwards for superimosing one or several curves.

Enter + (Addition). Choose a curve. Enter the constant, confirm. The new curve is displayed and stored temporarily under the name **SC (index)**.

13.5.4.7 Ratio

Without going through the multiple wavelength mode, it is possible to perform ratio calculations directly on the spectrum or spectra displayed.

-Press **F7 (Ratio)**.



a) With cursor

Press **F1 (Cursor)**.

Move the first cursor with the direction arrows.

Confirm.

The monitor displays the first wavelength (W1).

Move the second cursor.

Confirm.

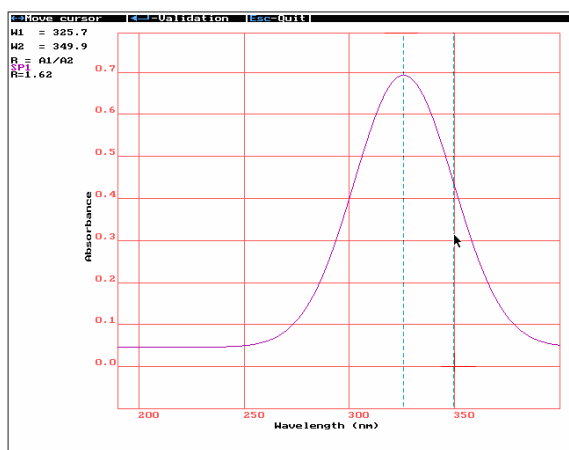
The monitor displays the second wavelength (W2) and the calculation formula $R = A1/A2$

A1: Absorbance at W1

A2: Absorbance at W2

R: Ratio

The software then gives the value of the ratio for each curve displayed



b) Manual

Press **F2 (Manual)**.

Enter both wavelengths. The results will be displayed as above.

For both modes (with cursor and manual):

Press **F3 (Printer)** for printing the results.

Press **F4 (Hardcopy)** for printing the results and the curve(s).

NOTE: For any other calculation to be performed on the absorbances of samples at different wavelengths, refer to the multiple wavelength mode in page 75

13.5.5 Note

The command **F4 (Note)** allows to write comments on the curves. The comments are not stored except if the user saves them under Image form (See in this chapter, Page 102).

Enter **F4 (Note)**. Place the cursor (initial position at the top right side of the screen below the strip display) by means of arrow keys or mouse. Confirm its position. Enter the text. Confirm.

For printing the curve(s) with comments, go to **F1 (I/O)** and enter **F5 (Hardcopy)**.

13.5.6 Windows

The command **F5 (Windows)** allows in the graphic mode to return to the parameters. The opposite operation is performed by entering **F4 (Graphic)**.

13.5.7 Absorbance

When a spectrum is in the transmittance mode on the monitor, this command allows to display it in the absorbance mode.

Press **F6 (Abs.)**.

13.5.8 Transmittance

When a spectrum is in the absorbance mode on the monitor, this command allows to display it in the transmittance mode.

Press **F7 (Trans.)**.

The processings which can be performed on a type of spectrum can also be performed on the other type

14 KINETIC MODE

NOTE: THE KINETIC MODE IS SIMILAR OF THE SPECTRUM MODE IN THE ORGANIZATION OF THE SUB-MENUS. WE WILL THUS REFER AT THIS PROGRAMS IN THE PRESENTATION OF THE SUB-MENUS

The kinetic mode is used for measuring the absorbance as a function of time. Example: determination of enzyme activity, evolution of the absorbance of a solution as a function of time...

On the main menu select "**Kinetic Mode**". Confirm.

Introduction of datas 2003/12/05 15:35:03

User's name	:	SMITH
Batch number	:	123
Origin	:	HOSPITAL
Kit number	:	5236

Esc A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Back
Space 0 1 2 3 4 5 6 7 8 9 + - * / . = % _ () [] ^ & * ~ Enter
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With the help of virtual keyboard or mouse, enter:

- The user's name (20 characters: signs, letters, numbers).
- The batch number (8 characters: signs, letters, numbers).
- The origin (30 characters: signs, letters, numbers).
- Kit number (8 characters: signs, letters, numbers).

These information are necessary for measurement traceability (ISO 9000, G.L.P,...) and will be printed with the results.

Press **ESC** to skip this step.

14.1 PROGRAMMING THE PARAMETERS

For the parameters modification, see page 36

F1-Execute F2-Parameters F3-File results Esc-Quit 2003/12/05 15:56:26

Kinetic mode v1.00

PARAMETERS		RESULTS
Wavelength (nm):	540	
Lag time (0-18000s):	60	
No of segments (1-100):	4	
Segment time (30-13000):	30	
Calculation:	Regre	
Decimal place (0-3):	0	
Factor (+/-10000):	1000	
Unit (Speed):	g/l	
Substrate unit (Micha):	uMol/l	
Numbering:	Auto	
Parameters locked:	No	

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With Esc key, it is possible to return to the previous menu and the main menu

-Press **F2 (Parameters)**, then **F1 (Modification)**.

*** Wavelength**

Choose from 190 to 900nm

*** Lag time (0-18000s)**

It is a time in seconds that must be introduced at the beginning of the analysis for taking into account the none linearity of a reading. The unit performs the scanning in the meantime but the slope calculation will be performed outside the lag time.

Choose from 0 to 18000s.

*** Number of segments (1-100)**

The measuring time can be cut into several segments to allow for intermediate slopes in the results.

Choose from 1 to 100.

*** Segment time (30-13000s)**

It is the time of each segment in seconds.

Choose from 30 to 13000 s.

Minimum time for calculating the slope.

1 segment x 30s = 30s

Maximum time for calculating the slope.

100 segments x 13000s = 1 300 000 s (about 361 hours)

*** Type of calculation**

**** Linear regression**

It is the most accurate means of calculating the slope for a linear variation.

When the unit performs a reading, it makes a least 300 scanings per second. For each second, the readings are averaged out.

The sequence of the absorbances forms a cloud of points between time T1 (beginning of the first segment) and time T2 (end of the last segment).

The calculation draws a straight line within the points by minimizing the square of the distances between themselves and the straight line. The result is obtained with the following formula:

$$Slope = \frac{(N \times \sum XY) - (\sum X \times \sum Y)}{(N \times \sum X^2) - (\sum X)^2} \times 60$$

N = total number of points of the kinetic curve (nb of segments x segment time)

$$\sum X = 1 + 2 + 3 + \dots + N = N(N+1)/2$$

$$\sum Y = \text{total of absorbances at points } 1, 2, 3, \dots, N = A1 + A2 + A3 + \dots + AN$$

$$\sum XY = (A1 \times 1) + (A2 \times 2) + (A3 \times 3) + \dots + (AN \times N)$$

$$\sum X^2 = 1 + 4 + 9 + \dots + N^2 = N(N+1)(2N+1)/6$$

The slope thus calculated is expressed in delta of Abs/min.

**** 2 Points**

The unit calculates the difference between the absorbances of the 2 most extreme points (end of the lag time and the end of the last segment).

$$R = \frac{\sum \Delta Abs \times Coef. \times 60}{N \times t_m}$$

ΔAbs : Absorbance at the beginning of segment minus absorbance at the end of the segment;

$\sum \Delta Abs$: Sum of absorbances delta of the segments.

N : Number of segments.

$Coef.$: Coefficient of molecular absorption.

t_m : Measuring time.

$60/t_m$: Ratio reducing the result to one minute.

The slope thus calculated is expressed in $\Delta Abs / mn$.
The result is report to one minute.

* Decimal places (0-3)

This parameter affects the resolution of the results.
Choose from 0 to 3

* Factor (+/-10000)

The factor can be negative. It is used for calculating the concentration. The result is obtained as follows:

$$Speed = \Delta Abs / mn \times Factor$$

* Unit (speed reaction)

Enter the abbreviation of the unit wanted.
i.e. U/l -n KAT/l -μKat/l...

* Unit (substrate concentration)

Enter the abbreviation of the unit wanted.
i.e.g/l - mg/l -μg/l - g/dl - μg/dl - mMOL/l - μMOL/l

* Numbering

Auto

The results will be in the form:

Sampl 1:

Sampl 2:

...

Unit

Allows to assign a name to the sample.

* Locked parameters

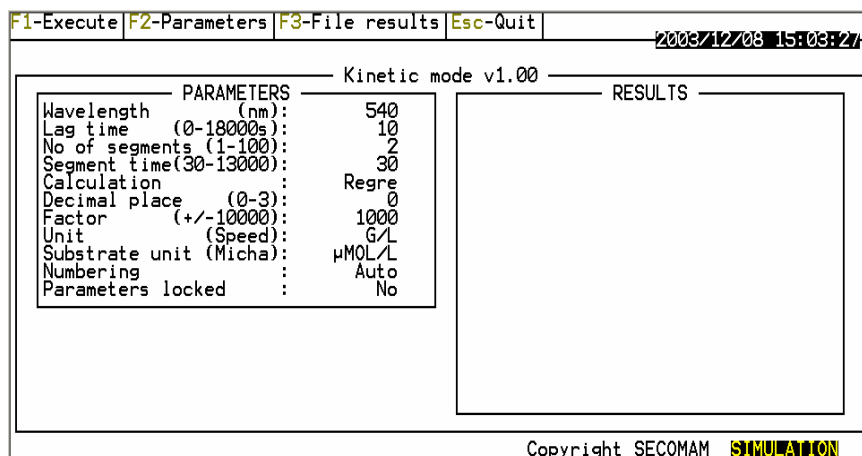
Allow to lock the analysis parameters: YES or NO. See page 90

14.2 PRINTING THE PARAMETERS

Press **F2 (Printer)** for printing out the parameters.

14.3 SAVING THE METHOD

Press **F3 (Save)** to save the parameters.



14.4 SAVING THE ASCII FILES

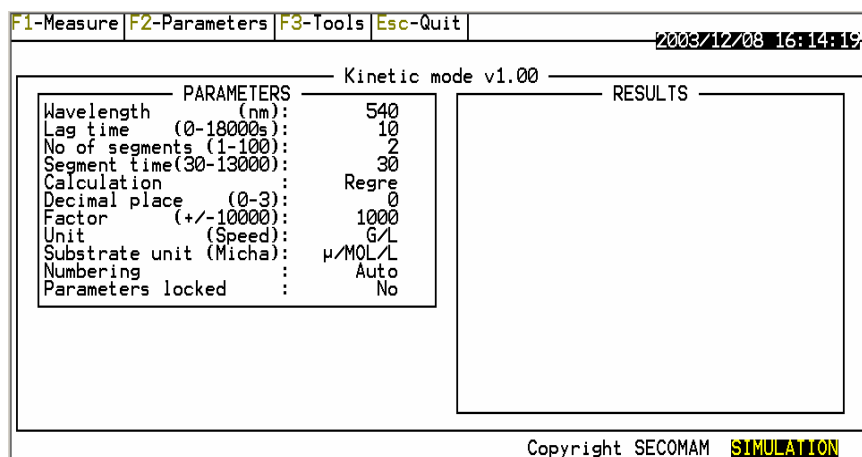
Offer the possibility to keep the results of the analyses in the form of ASCII files.

Press F3 (File results) and enter the file name under 8 characters.
See the explanation page 86

NOTE: If the operator has failed to assign a name to a file for storing the data of a reading, the software creates a file by default call KINET.PRN. The data stored formerly will be overlaid by the new ones upon each reading.

14.5 MEASUREMENT

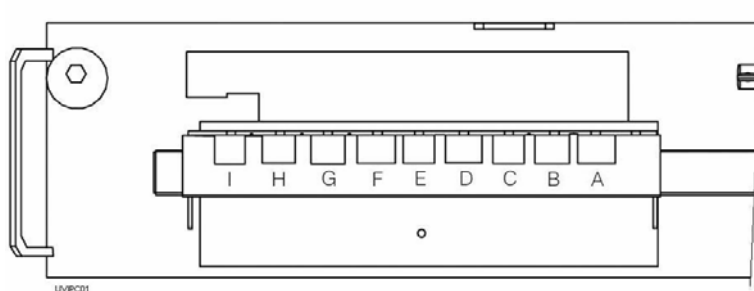
Press F1 (Execute)



Prepare the multi-cell holder as follows:

Position A: Blank (reagent) or reference
Position B through I: Samples

Throughout the measuring sequence, the multi-cell holder will be prepared in the same way.



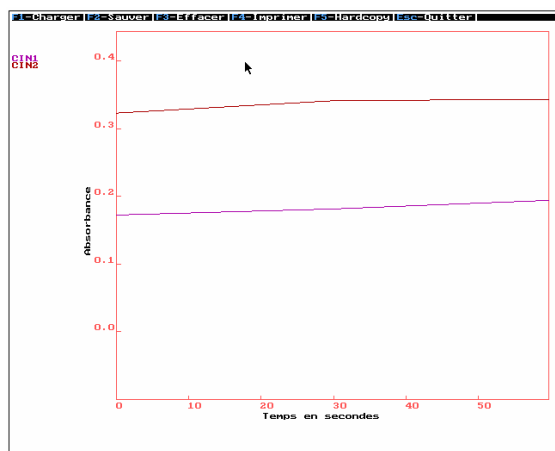
Press **F1 (Measure)**. - Enter the number of samples to be measured. Confirm.

The spectrophotometer will make the measurement, every 30 seconds of the samples and the reference (in A position) compensating, at the same time, an eventual unit or reference drift.

The curves are drawn on the screen following data acquisition.

They will be saved temporarily under the name **KIN (index)**.

The name with the higher index will be the last scan performed by the operator.



At the end of the reading, the result is printed out in the following form:

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi Light v1.00
 Date: Friday november the 21,2003 Time: 11:43 am
 User's name: SMITH
 Batch number: 123
 Origin: HOSPITAL
 Kit number: 1256

Method: Kinetic Mode v1.00

1) Sam. 1 Time: 11:43 am
 2) Speed = 18 G/L
 3) Slope = 0.018 Abs / mn
 4) time 5 sec Abs. = 0.174 Slope = 0.020 Abs/mn
 5) time 35 sec Abs. = 0.184 Slope = 0.017 Abs/mn

1) Sam. 2 Time: 11:43 am
 2) Speed = 18 G/L
 3) Slope = 0.018 Abs / mn
 4) time 5 sec Abs. = 0.326 Slope = 0.034 Abs/mn
 5) time 35 sec Abs. = 0.343 Slope = 0.000 Abs/mn

Result explanation:

- Line 1: Sample name.
- Line 2: Reaction speed is the total slope per minute multiplied by K factor.
- Line 3: Total slope per minute.
- Line 4, 5, Starting time for every segment, the corresponding absorbance and intermediate slopes reduced to one minute for visualizing the kinetic evolution.

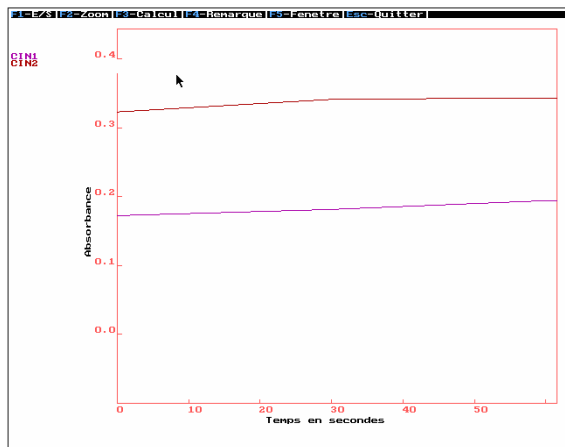
To display the results, enter **F3 (Tools)**, then **F5 (Windows)**.

F1-I/O	F2-Scales	F3-Calculation	F4-Graphic	Esc-Quit	2003/12/08 16:47:58
Kinetic mode v1.00					
PARAMETERS Wavelength (nm): 540 Lag time (0-1800s): 5 No of segments (1-100): 2 Segment time(30-13000): 30 Calculation : Regre Decimal place (0-3): 0 Factor (+/-10000): 1000 Unit (Speed): G/L Substrate unit (Micha): $\mu\text{MOL/L}$ Numbering : Auto Parameters locked : No			RESULTS Sam 1 Time : 4:46 pm Speed = -51 G/L Slope = -0.051 Abs/mn time 5 sec Abs. = 0.223 Slope = -0.068 Abs/mn time 35 sec Abs. = 0.189 Slope = -0.026 Abs/mn Sam 2 Time : 4:46 pm Speed = 73 G/L Slope = 0.073 Abs/mn time 5 sec Abs. = 0.338 Slope = 0.002 Abs/mn time 35 sec Abs. = 0.339 Slope = 0.145 Abs/mn		
Copyright SECAMAM SIMULATION					

IMPORTANT: To avoid loosing the curve in process due to a power failure or an accidental exit from the kinetic program, the ANTHELIE Data saves it automatically every minute and stores it under the name **LAST (index)**.

14.6 TOOLS

Press **F3 (Tools)**.

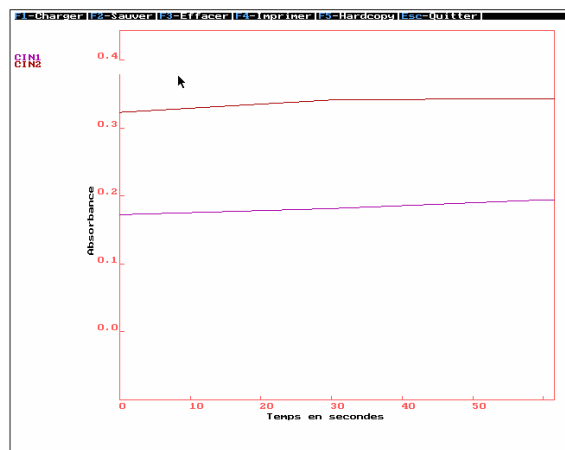


This sub-routine is used for various processings (zoom, derivative,...) or calculation on the curves stored in memory.

14.6.1 Input/Output

This function allows to load, save, delete, and print one or several curves.

Press **F1 (I/O)**.



14.6.1.1 Save

The curves may be saved one by one. The curves may also be saved one or several together with some comments (so we speak about image)

NOTE: THE IMAGES ARE DIFFERENT FROM CURVES AND IT IS NOT POSSIBLE TO SUPERPOSE BETWEEN THEM OR WITH CURVES.

a) Curves saving

Maximum curve saving capacity on hard disk: 1500 kinetic curves. It is possible to increase the memory storage capacity by using the "save" routine which allow to export or import curves on a diskette. See explanations page 80.

Press **F2 (Save)**, then **F1 (Curve)**.

No curve must be saved, return to the previous menu. Otherwise choose the curve(s) to be stored among the curves drawn. Confirm. Enter the name in 8 letters, confirm. Return to the previous menu.

b) Images saving

Maximum image saving capacity on hard disk: 1500 images.

Press **F2 (Save)**, then **F2 (Image)**.

Enter the name in 8 letters, confirm.

NOTE: It is advised to write as a comment, the image file name

14.6.1.2 Load

This function is used for loading one or several curves (up to 9) on the screen, for various processings (zoom) or calculations (derivatives, operations, slopes,...).

NOTE: Upon the first entry in the kinetic analysis mode and after loading the tool function, the display strip shows **Load**, **Calculation** and **ESC**.

If kinetic curves have been saved, it is possible to load one or several of them. If there is no kinetic curve in the memory, the functions **Load** and **Calculation** loop back.

Return to the previous menu with the **ESC** key.

a) Curves loading

Press **F1 (Load)**, then **F1 (Curve)**.

In the kinetic curves library proposed, the spectra saved (ASSAY01-SAMPLE03) and the kinetic curve recently performed (KINxx) are of different colors.

The later will be deleted as soon as kinetic mode is closed. Choose the curve(s) to be loaded, confirm and confirm.

B) Images loading

Press **F1 (Load)**, then **F2 (Image)**.

In the images library proposed, choose the one to recall, confirm and confirm.

14.6.1.3 Delete

This function allows to delete one or several curves chosen by the user.

Press **F3 (Delete)**.

Choose the curve(s) to be deleted, confirm and confirm.

The curve(s) will be deleted.

14.6.1.4 Print

-Press **F4 (Print)**.

The curve(s) will be printed horizontally without comments in a 11x21cm format.

14.6.1.5 Hardcopy

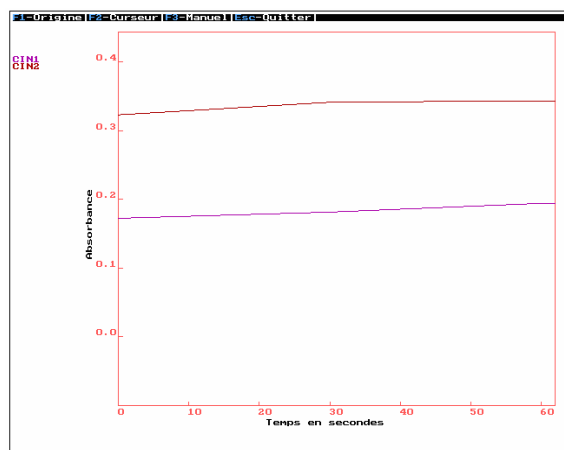
Press **F5 (Hardcopy)**.

The curve(s) will be printed vertically without comments in a 21x29.7 cm format.

14.6.2 Scales

This function allows to expand an interesting section of a curve.

-Press **S (Scales)**.



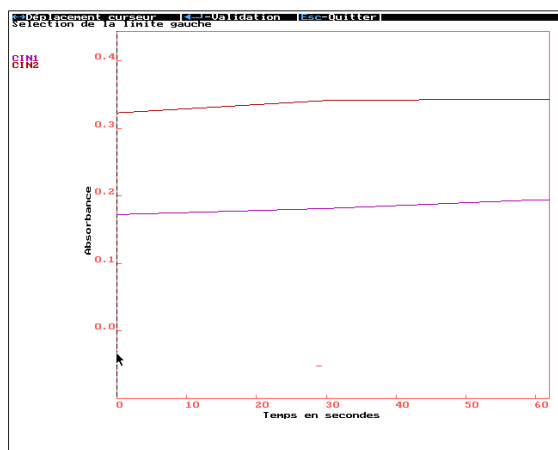
NOTE: Throughout the function , the ESC key allows to return to the previous menu.

14.6.2.1 Original

This command allows to return to the initial curve after a manual expansion or with the cursor.
Press **F1 (Original)**.

14.6.2.2 Zoom with cursor

Press **F2 (Cursor)**.

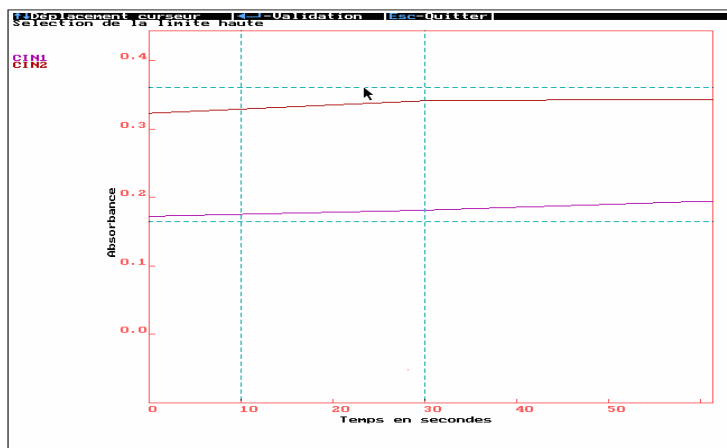


Select the left limit of the selection to be expanded by moving the cursor with the ← and → keys. Confirm.

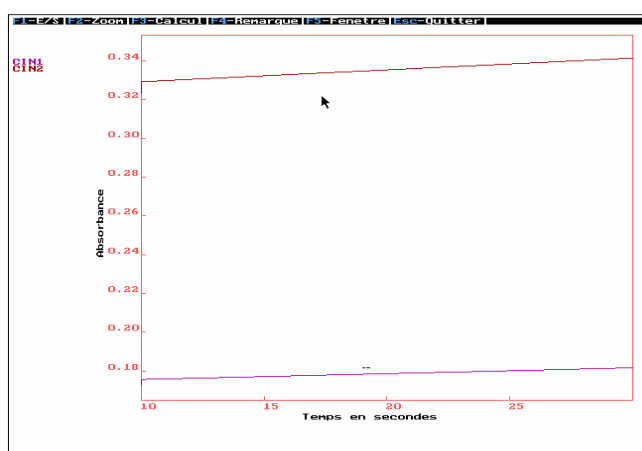
Then select the right limit of the selection to be expanded

Frame at the top and at the bottom the section to be expanded by moving the cursor with the ↓ and ↑ keys and validating whenever it reaches the correct position.

Example:



Confirm.



To retrieve the initial curve, enter **F1 (Original)**.

14.6.2.3 Manual zoom

Press **F3 (Manual)**.

Enter the time scales.

Example:

Time mini = 10. Confirm

Time maxi = 20. Confirm

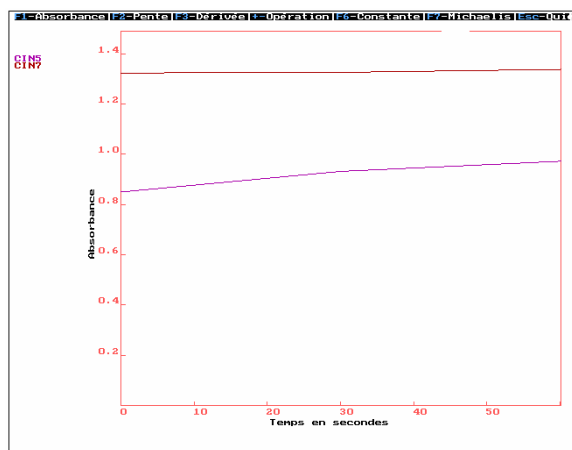
Automatic zoom?

Yes: The unit recalculates the absorbance scales automatically.

No: Enter the absorbances scales.

14.6.3 Calculation

Press **F3 (Calculation)**.



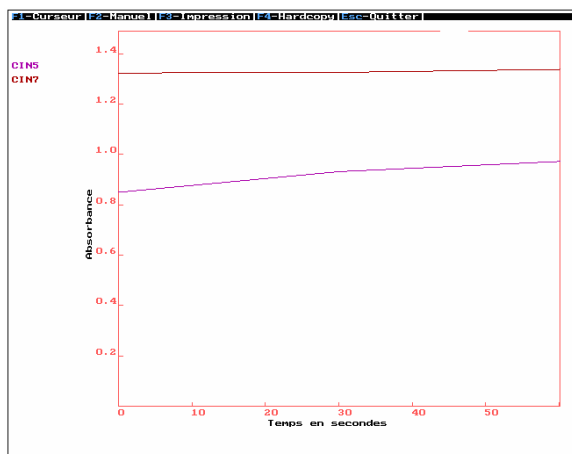
This function allows to :

- read the absorbance on one or several curves at a given time
- calculate a slope.
- calculate the derivatives
- add two curves
- subtract one curve from another
- multiply a curve by a number
- add a constant to a curve
- calculate the Michaelis constant.

14.6.3.1 Absorbance

Allows to read an absorbance in view of a time on one or several spectra.

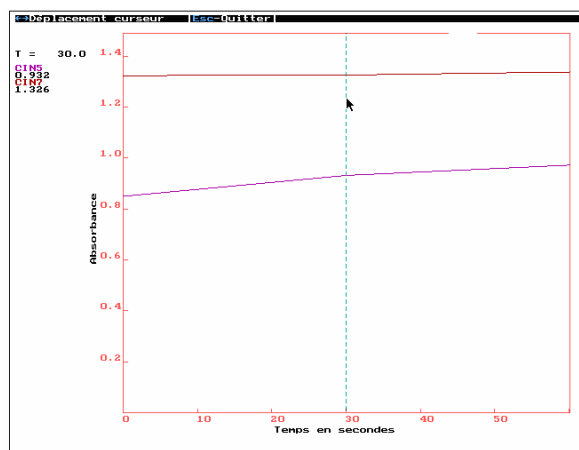
Press **F1 (Absorbance)**.



a) With cursor

The absorbance of one or several curves can be read simultaneously depending on the position of a cursor moved by the operator.

Press **F1 (cursor)**.



At the top of the screen, the time in seconds, the name of each curve and the absorbance corresponding to such time below are displayed. It is possible to change the position of the cursor by means of the ← and → keys. With each new position of the cursor, new Time/Absorbance couples are displayed.

b) Manual

Press **F2 (manual)**.

Enter time in seconds. The unit will display the absorbance value for the curve(s) visualized on the monitor.

For both modes (with cursor and manual), the command **F4 (Hardcopy)** allows to print the curve(s) with the values. The command **F3 (Print)** only print out the values as follows.

Time = 20.0
Sam. Abs. = 0.904
Sam. Abs. = 1.325

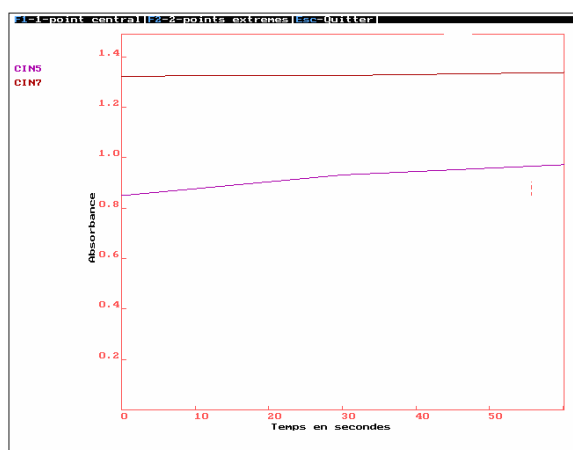
Press **ESC** to return to the previous menu.

14.6.3.2 Slope

This function allows to read the slope reduced to one minute and multiplied by the coefficient indicated in the parameter window. Such calculation can be performed in the regression or 2-point mode, between 2 times entered by the operator or with reference to a central point around which the operator will have defined a time range on one or several curves.

Download the curve(s) on which slope calculations are to be performed.

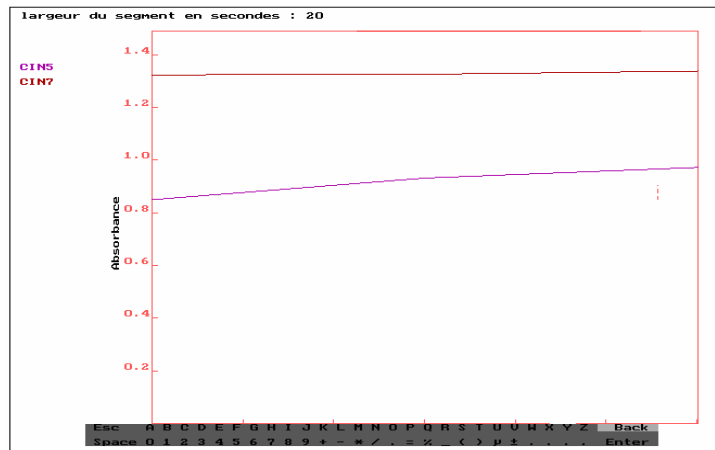
Press **F2 (Slope)**.



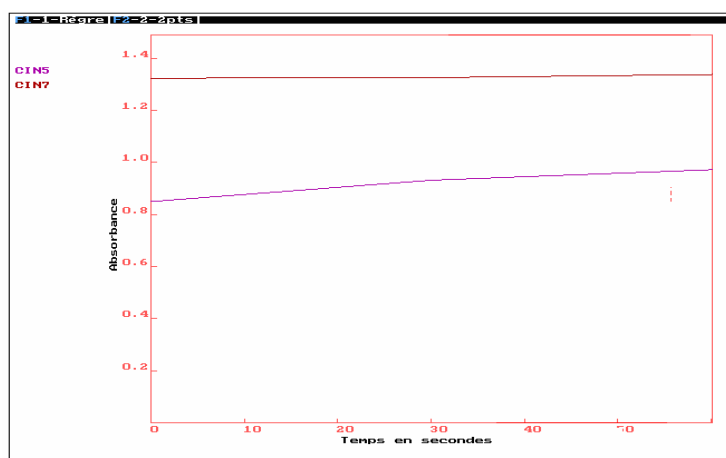
a) Central point

The operator is to define a time range in seconds which will be centered automatically around the measuring point. Example:20 sec.

Press **F1 (Central point)**.

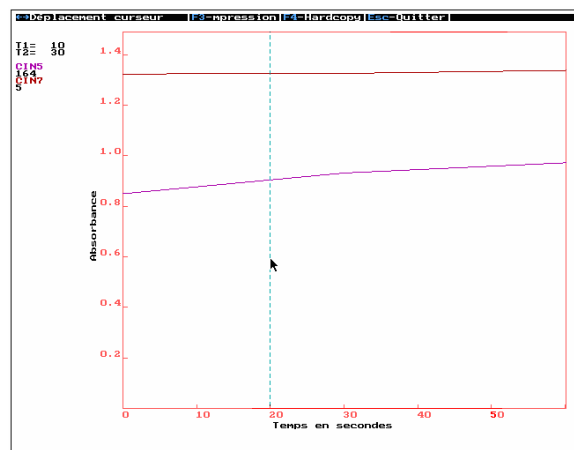


He will then choose the calculation mode: regression or 2-point. **F1 (Regre)** or **F2 (2pts)**.



He will just have to move the cursor with the direction keys.

The software will automatically compute the slope on one or several curves within the time range centered around the position of the cursor.



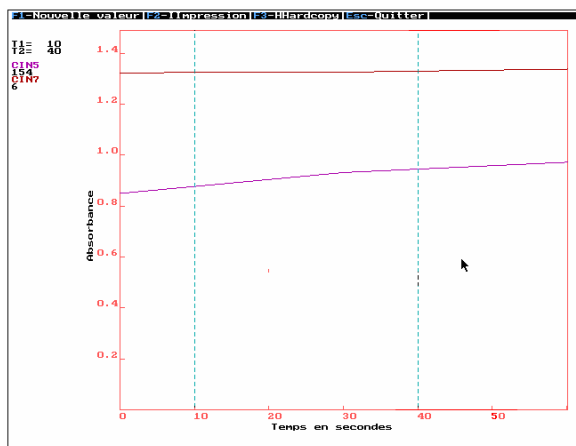
Both times defined by the time range will be displayed together with the name(s) of the curves and the slope(s). They are calculated with the last coefficient displayed in the parameter window and reduced to one minute.

b) Extreme points

Press **F2 (Extreme points)**.

Set the times with the cursors. Confirm.

Choose the calculation mode: regression **F1 (Regre)** or 2 points **F2 (2pts)**. Confirm.



Both times defined by the times range are displayed with the name(s) of the curves and the slope(s).

They are calculated with the last coefficient displayed in the parameter window and reduced to one minute.

The command **F1 (New value)** allows to select other time intervals.

For both modes (central point or Extreme points) the command **F2 (Print)** allows to print the result.

The command **F3 (Hardcopy)** prints out the curve(s) with the results.

14.6.3.3 Derivatives

Derivate a kinetic curve allows to see the slope evolution versus time.

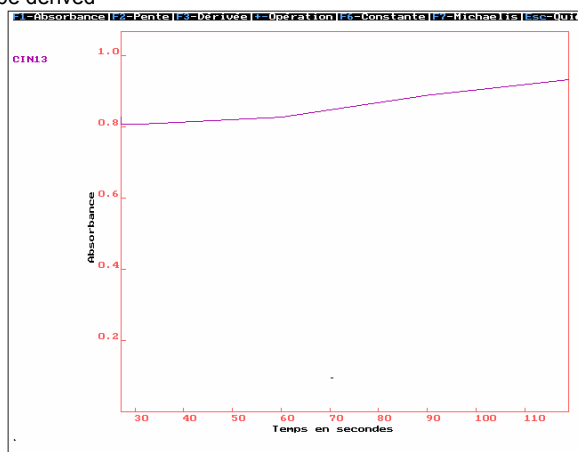
* CALCULATION OF DERIVATIVES

Same calculation as spectrum mode.

See page 98

Press **F3 (derivative)**.

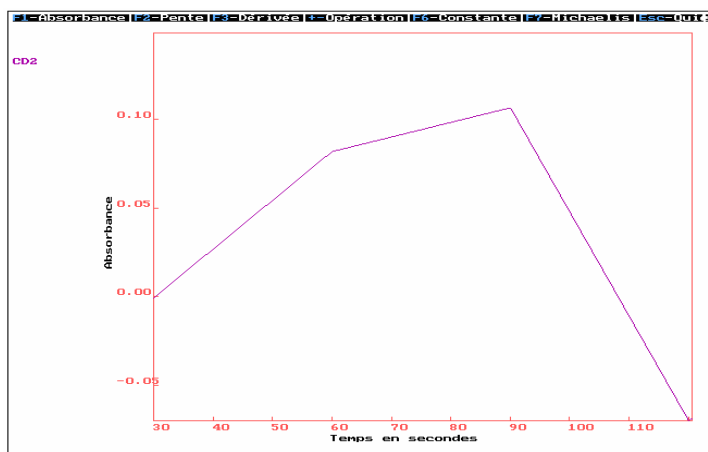
Choose the kinetic curve to be derived



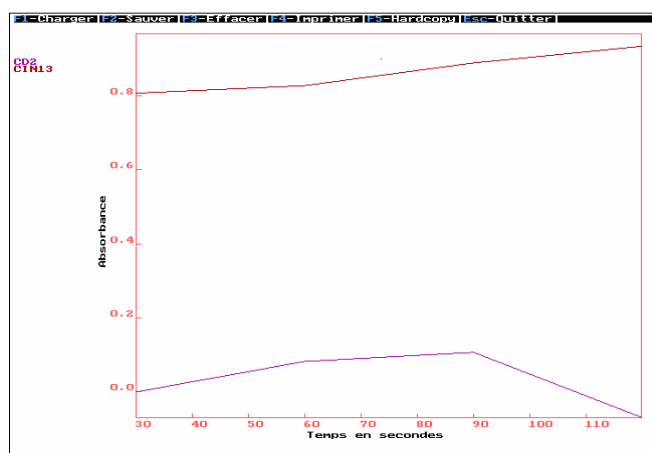
Choose the order of the derivative and the differentiation step.

The step expressed in seconds corresponds to the width of the smoothing window.

Example: Kinetic : KIN13
 Order : 1
 Step : 7s



The derived curve is saved temporarily under the name **CD (index)** and may be retrieved for superimposition with the initial spectrum.



14.6.3.4 Addition

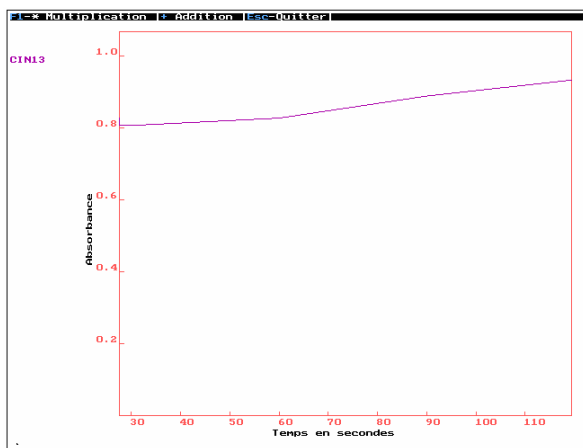
Allows to adds two curves. Enter **+** (**+ - Operation**). Choose the first curve, confirm. Choose the second curve, confirm. The new curve is displayed and temporarily stored under the name **KINA (index)**.

14.6.3.5 Substraction

Allows to subtract one curve from another. Enter **-** (**+ - Operation**). Choose the first curve, confirm. Choose the second curve, confirm. The new curve is displayed and temporarily stored under the name **KINA (index)**.

14.6.3.6 Constant

Press **F6 (Constant)**.



a) *Multiplication

Allows to multiply a curve by a positive or negative number. Enter * (**multiplication**). Choose the curve. Enter the multiplying coefficient and confirm. The new curve is displayed and stored temporarily under the name **KINM (index)**.

b) +Addition

Allows to add a positive or negative constant to the curve to shift it upwards or downwards for superimposing one or several curves. Enter + (**Addition**). Choose a curve. Enter the constant, confirm. The new curve is displayed and stored temporarily under the name **KINC (index)**.

14.6.3.7 Km calculation (Michaelis constant)

We have n measurements of enzymatic reaction speed obtained by the variation of substrate concentration (enzyme concentration is constant).

We obtain couples of values as follow:

$$(S_1, V_1), (S_2, V_2), (S_3, V_3), \dots (S_n, V_n).$$

Michaelis and Menten equation:

$$V = \frac{V_m \times [S]}{K_m + [S]}$$

V : Reaction speed ($\Delta Abs / mn$).

$[S]$: Substrate concentration.

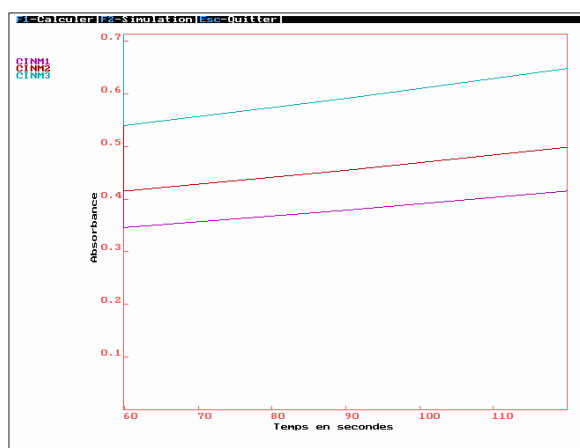
K_m : Michaelis and Menten constant (inverse ratio to the affinity of enzyme for the substrate).

V_m : Maximum reaction speed (When $[S] \rightarrow \infty$).

-Proceed to the various kinetics acquisition for various substrate concentrations.

Example of 3 samples

Press **F3 (Tools)**, **F3 (Calculation)**, then **F7 (Michaelis)**.



Press **F1 (Calcul)**, choose the first kinetic curve, then confirm and confirm. Enter the corresponding substrate concentration.

Proceed in the same way for the other kinetic curves.

After the selection, it will display (Woelf-Hanes form) the Michaelis and Menten equation curve.

It will print the value of K_m as follows.

SCHOTT INSTRUMENTS, UV-VIS Spectrophotometer Uvi
Light v1.00
Date: Friday november the 21,2003 Time: 11:43 am
User's name: SMITH
Batch number: 123
Origin: HOSPITAL
Kit number: 1256

Method: KINETIC Mode v1.00

Sam. 1 Time: 11:43 am
Conc = 20 µMOL/L
Speed = 494 UI/l
Slope = 0.494 Abs/mn
Time 5 sec Abs. = 0.546 Slope = 0.671 Abs/mn
Time 15 sec Abs. = 0.658 Slope = 0.517 Abs/mn
Time 25 sec Abs. = 0.744 Slope = 0.429 Abs/mn
Time 35 sec Abs. = 0.815 Slope = 0.387 Abs/mn

Michaelis constante: Km = 5 µMOL/L

a) *Woolf-Hanes form*

Press **F2** (*Woolf-Hanes*).

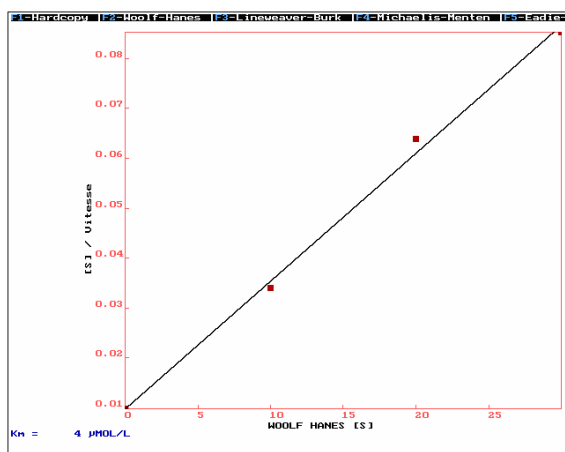
$$\frac{[S]}{V} = \frac{K_m}{V_m} + \frac{1}{V_m} [S]$$

On Y axis $[S]/V$.

On X axis $[S]$.

Slope = $1/V_m$.

Bias = K_m/V_m .



K_m value is displayed on the bottom left side of the screen.

b) *Lineweaver-Burk form*

Press **F3** (*Lineweaver-Burk*).

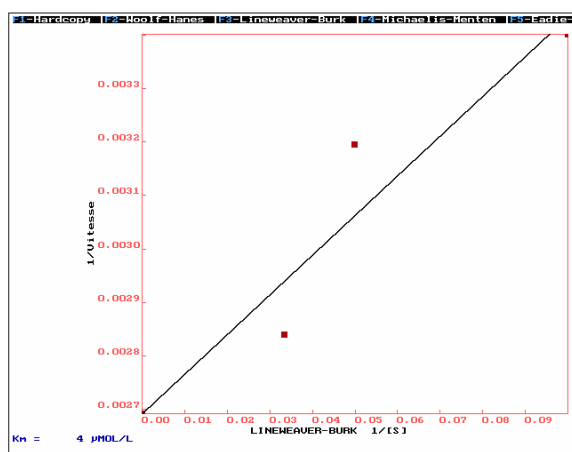
$$\frac{1}{V} = \frac{K_m}{V_m} \times \frac{1}{[S]} + \frac{1}{V_m}$$

On Y axis $1/V$.

On X axis $1/[S]$.

Slope = K_m/V_m .

Bias = $1/V_m$.

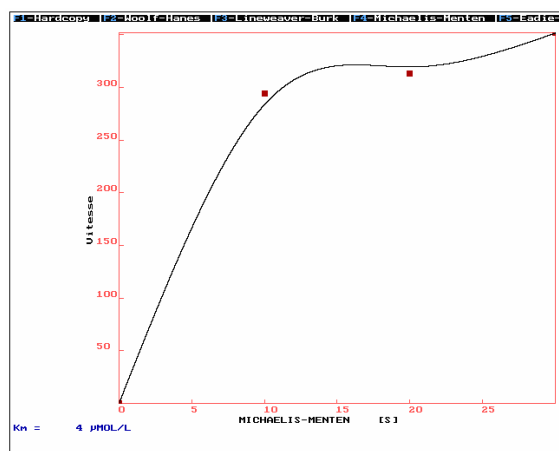


c) Michaelis-Menten form
Press **F4** (Michaelis-Menten).

On Y axis V .

On X axis $[S]$.

$$K_m = [S] \text{ when } V = V_m/2$$



d) Eadie-Hofstee form
-Press **F5** (Eadie-Hofstee).

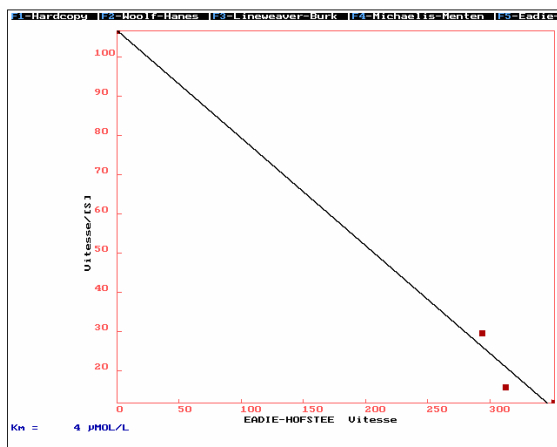
$$\frac{V}{[S]} = -\frac{V}{K_m} + \frac{V_m}{K_m}$$

On Y axis $V/[S]$.

On X axis $[V]$.

Slope = $-1/K_m$.

Bias = V_m/K_m



Press **F1 (Hardcopy)**. It prints the curve and the Michaelis constant value.

Press **ESC (ESC-Quit)**. It prints the Michaelis constant value and comes back to the previous menu.

e) Simulation

The user can rebuilt the curve $[S/V = f([S])]$ and automatically calculate Michaelis constant.

-Press **F2 (Simulation)**, enter the points number with, for every one, the substrate concentration and the reaction speed.

It will display the curve and the Michaelis constant value.

Proceed the same to print the curve and the constant value.

f) Error messages

Problem 8: The substrate concentration values are not increasing and regular

$$X1 < X2 < X3 < \dots < Xn$$

Problem 9: The reaction speed values are not increasing and regular.

$$Y1 < Y2 < Y3 < \dots < Yn$$

14.6.4 Note

The command **F4 (Note)** allows to write comments on the curves. These comments are not stored except if the user saves them under image form.

Enter **F4 (Note)**. Place the cursor (initial position at the top right side of the screen below the strip display) by means of the direction keys. Confirm its position. Enter the text. Confirm.

To print the kinetic curve(s) with comments, press **F1 (I/O)** and **F5 (Hardcopy)**.

14.6.5 Windows

The command **F5 (Windows)** allows in the graphic mode to return to the parameters. The opposite operation is performed by entering **F4 (Graphic)**.

15 MACRO-COMMANDS

WARNING: These commands are available, only if an external alphanumeric keyboard is connected.

The software allows for the creation of macro-commands by the operator.

Such macro commands record a combination of keys. The software will reproduce automatically such combinations in the order in which the operator has recorded them.

Macro-commands help to save time when a long or repetitive task is to be performed.

It is for example possible in the spectral analysis program, after setting the baseline, to measure the spectrum of a sample, to search automatically for peaks, to draw the derivative and to print values plus curves.

It is easy to see that, if operations must be performed on some twenty samples, a macro-command reproducing such sequence of operations will be welcome.

It is also possible to repeat such macro-commands a number of times and to set parameters for the interval in between two repetitions.

15.1 CREATION OF A MACRO-COMMAND

For creating a macro-command in a user program:

- Enter the analysis mode concerned.
- Go straight to the point in the program where the macro-command begins
- Press keys **Ctrl** and **F1**.

It will display at the left top of the screen, the following message:
"Beginning of the macro"

Then run the sequence of commands.

Ex:

- Draw the spectrum of the sample.
- Print the curve
- Draw the automatic list of peaks with a difference of more than 0.1 Abs
- Print the value of the peaks
- Draw the derivative of order 1 with a differentiation step of 5nm
- Print the derivative curve.
- **Return to the place where the macro-command begun.**
- Press the **Ctrl** and **F2** keys.

It will display at the left top of the screen, the following message:
"End of macro: hit a control key"

Assign a function key to the macro-command.
Which keys can the operator use?

Keys **Alt F1** through **Alt F10**.

For this example, we have chosen **Alt F1**.

Once the key has been assigned, It will display at the left top of the screen, the following message:
"Name of macro"

Enter the name of the macro-command (up to 18 letters and figures). Ex: SPECTRUM MEAS.

15.2 EXECUTION OF A MACRO-COMMAND

For launching a macro-command:
Enter the mode of analysis concerned.
In our example: SPECTRUM mode.

Go to the point where the macro-command begins.

Press the function key assigned to the macro-command.

In our example: **Alt F1**.

The above mentioned sequence of commands will be run and the unit will return to the point of departure. The operator may either launch the macro-command again or use the commands directly.

15.3 RATED EXECUTION OF A MACRO-COMMAND

It may be useful to repeat the same macro-command at a specific interval.

For repeating a macro-command on a rated basis:

Enter the mode of analysis concerned.

In our example: SPECTRUM mode.

Go to the point where the macro-command begins.

Press the **Ctrl** and **F3** keys.

It will display at the left top of the screen, the following message:

"Hit a macro key"

In our example: **Alt F1**.

It will display at the left top of the screen, the following message:

"Repeat"

Enter the number of times (from 2 to 1000) the macro-command must be run.
Confirm.

It will display at the left top of the screen, the following message:

"time between to macros (in sec):"

This time corresponds to the interval **between two beginnings of macro-command**.

Enter a time between 0 and 30 000 seconds.
Confirm.

The sequence is run as follows:

- Execution of the macro-command
- Discounting of the time remaining after executing the macro-command
- New launching of the macro-command.

NOTE: If the execution time of the macro-command is superior to the preset interval, the software will repeat the macro-command.

NOTE: To escape out the macro-command, press **"Esc"**.

15.4 RECALL OF APPLICATION AND LISTING OF A MACRO-COMMAND

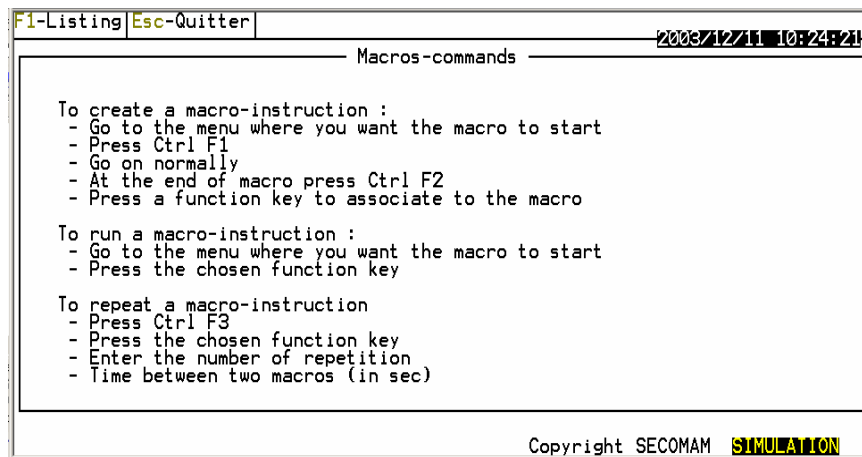
15.4.1 Recall of application

From the main menu, enter **F3 (Tools)**.



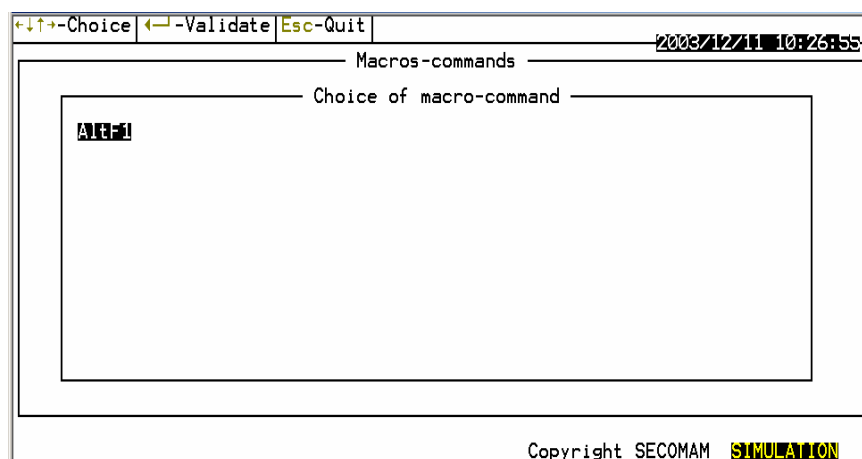
Enter **F2 (Macros)**

The software displays the procedure to be used for creating, retrieving and running the macro-command in a rated fashion.

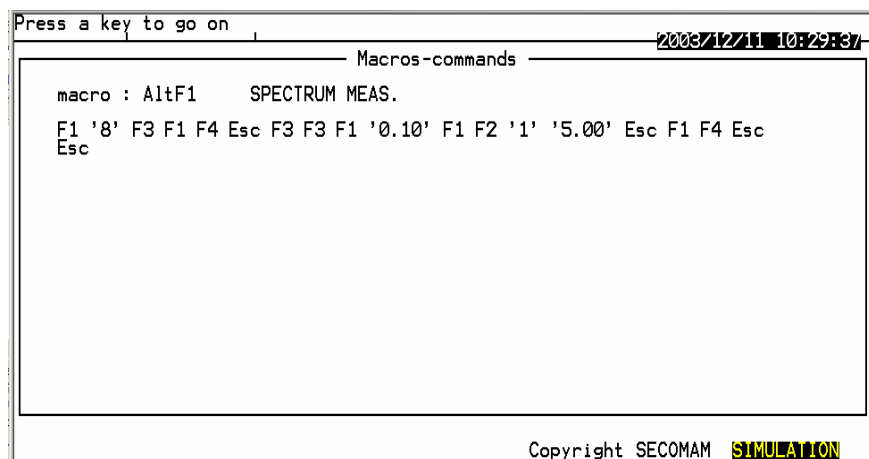


15.4.2 Listing of macro-commands

Enter **F1 (Listing)**.



Select the macro-command to be listed.
Confirm and confirm.



The key(s) associated to the macro-command, its name and the corresponding sequence of commands are displayed.

In our example: **Key Alt F1**, name SPECTRUM MEAS..

F1 = Measure
'8' = Number of cuvettes
F3 = Tools
F1 = I/O
F5 = Hardcopy
Esc = Quit
F3 = Calculation
F3 = Maxi
F1 = Peaks
'0.10' = Difference between the peak and the valley
F1 = Printer
Esc = Quit
F4 = Graphic (return to the curve)
F3 = Calculation
F2 = Derivative
'1' = Order of the derivative
'5.00' = Differentiation step
ESC = Quit
F1 = I/O
F5 = Hardcopy
Esc = Quit

Press any key to return to the main menu.

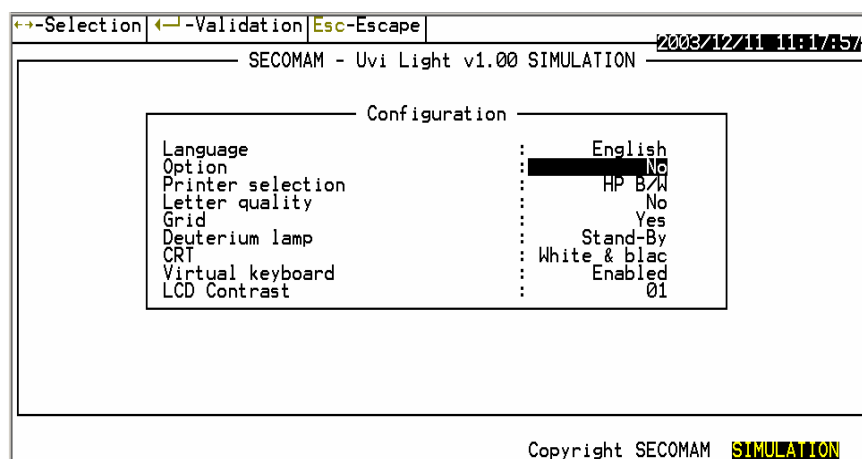
16 UTILIZATION AS A SINGLE CELL HOLDER

To install this accessory, refer to the Uvi Light installation guide

It is possible to use the multicell holder as a single cell holder without to remove it (working with a flow through cell).

To do that, proceed as follows:

From main menu, press **F1 (Config)**.

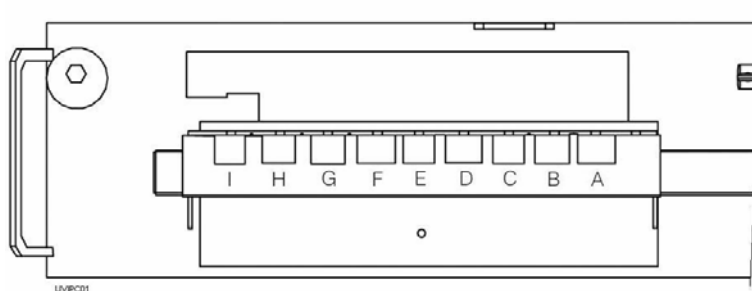


Change "**Option**" parameter.

Choose "**No**".

Confirm all window parameters.

The spectrophotometer positions the A compartment of the multicell holder right into the beam.



In that configuration, only position A can read the measuring cell.

The operator alternates the reference solution, the blank, the standard and the sample as requested by the spectrophotometer.

The type of holder used is displayed at the bottom of the screen.

NOTE: Upon starting the unit, if the "No" option has been selected, the spectrophotometer will check if there is a multicell holder installed and will move the A position right into optical beam.

17 FILES

17.1 FILES DESCRIPTION

17.1.1 Program files

They incorporate the measuring programs created by the operator. They may be run directly from the main menu.

These methods can be copied on floppy disk and be filed for ulterior use.

The parameters of a program can be retrieved from the DOS by entering (Name of the program).PLN.

Ex: **PROT.PLN**

In the main menu, programs will appear as follows:

First left column: Name of the method assigned by the operator.

Second column: Name of the file assigned by the operator.

Example:

Proteins measurement.....PROT

17.1.2 Editor files

The **SPECTRO PASCAL** software is a language derived from the PASCAL already developed by SCHOTT INSTRUMENTS.

It consists of macro instruction commands such as: Init window, Measure Absorbance...

Instructions in **SPECTRO PASCAL** can be found in each of the editor programs. To use such programs, they must be compiled beforehand. This is why there may appear a number of names of editor programs which the operator cannot find in the main menu.

They have not been compiled.

These programs can be copied on floppy disk and be filed for ulterior use.

These programs may be retrieved from the DOS by entering (Name of the program).TEX.

Ex.: **MEASURE.TEX.**

In the menu of editor programs, they will appear under the name assigned to them by the operator or by SCHOTT INSTRUMENTS.

Ex.: **MEASURE**

17.1.3 Spectra files

They include, in an encoded form, the data of the spectra stored.

These files can be copied on floppy disk and be filed for ulterior use.

These files may be retrieved from the DOS by entering (Name of the file).SPE

Ex.: **HOLMIUM.SPE**

In the menu of spectra files, they appear under the name assigned to them by the operator.

Ex.: **HOLMIUM**

17.1.4 Kinetic files

They include, in an encoded form, the kinetic data which have been stored.

These files can be copied on floppy disk and be filed for ulterior use.

These files may be retrieved from the DOS by entering (Name of the file).CIN

The extension for such files is ".CIN".

Ex.: **SAMPLE.CIN**

In the menu of kinetic files, they appear under the name assigned to them by the operator.

Ex.: **SAMPLE**

17.1.5 Image files in spectrum mode

An image, in scan mode, is the screen representation where the spectra are displayed. It may contain one or several curves with comments or not.

These files can be copied on floppy disk and be filed for ulterior use.

These files may be retrieved from the DOS by entering (Name of the file).IMS

Ex.: **IMAGE1.IMS**

In the menu of image files in spectrum mode, they appear under the name assigned to them by the operator.

Ex.: **IMAGE1**

17.1.6 Image files in kinetic mode

An image, in kinetic mode, is the screen representation where the spectra are displayed. It may contain one or several curves with comments or not.

These files can be copied on floppy disk and be filed for ulterior use.

These files may be retrieved from the DOS by entering (Name of the file).IMC

Ex.: **IMAGE2.IMC**

In the menu of image files, they appear under the name assigned to them by the operator.

Ex.: **IMAGE**

17.1.7 ASCII files

They include in the ASCII format, the results of readings if the operator has caused them to be saved. They also include in the ASCII format the spectra or kinetic curves which have been converted by sub-routine **F3-(Tools)**, **F1 (Files)** and **F4 (Curve→ASCII)**.

Such data may be copied on floppy disks and operated by other software (Excel, ...).

These files may be retrieved from the DOS by entering (Name of the file).PRN

Ex.: **RESULTS.PRN**

In the menu of the ASCII file, they appear under the name assigned to them by the operator.

Ex.: **RESULTS**

17.1.8 Macro files

It includes in an encoded form the sequence of commands which make up the macro instructions.

These files can be copied on floppy disk and be filed for ulterior use.

These files may be retrieved from the DOS by entering (Name of the file).MAC

In the menu of the Macrofile, they appear under the name of the key used for storing them.

Ex.: **ALTf1.MAC**

In the menu of the macro file, they appear under the name assigned to them by the operator.

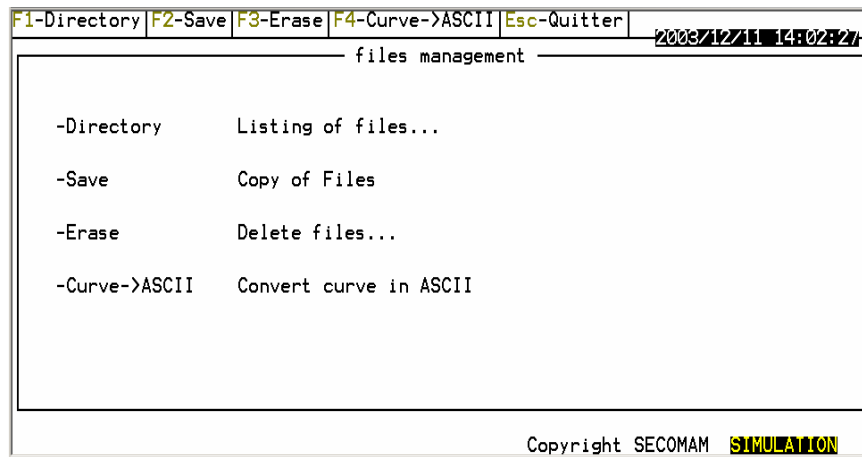
Ex.: **AltF1**

17.2 FILES SUB-ROUTINE

From the main menu, press **F3 (Tools)**.

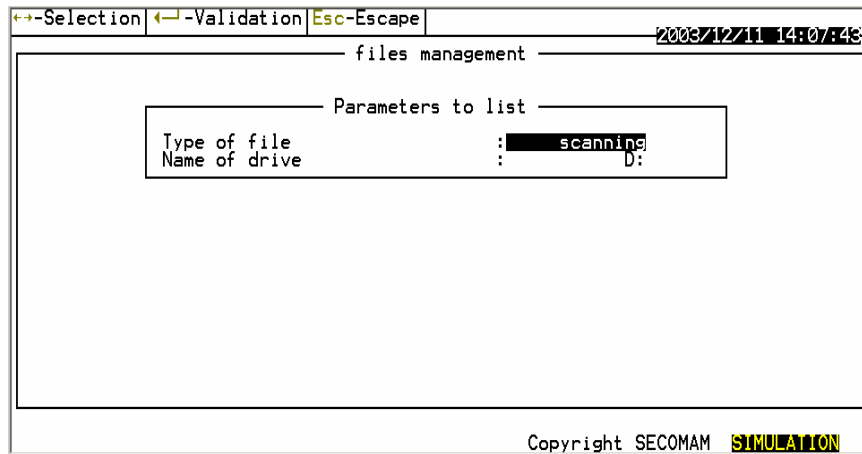


Press **F1 (Files)**.



17.2.1 Directory

This function is used for displaying the list of files from hard disk or floppy disk
Press **F1 (Directory)**.

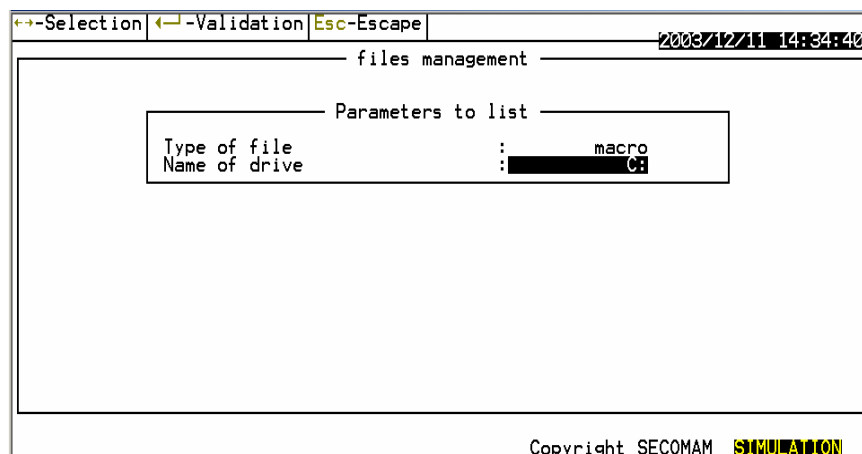


Type of file: Search for the type of file to be displayed with the Suppr/Del key and the ← and → keys. There are eight kinds of files: refer to the beginning of chapter for the description of files. Confirm.

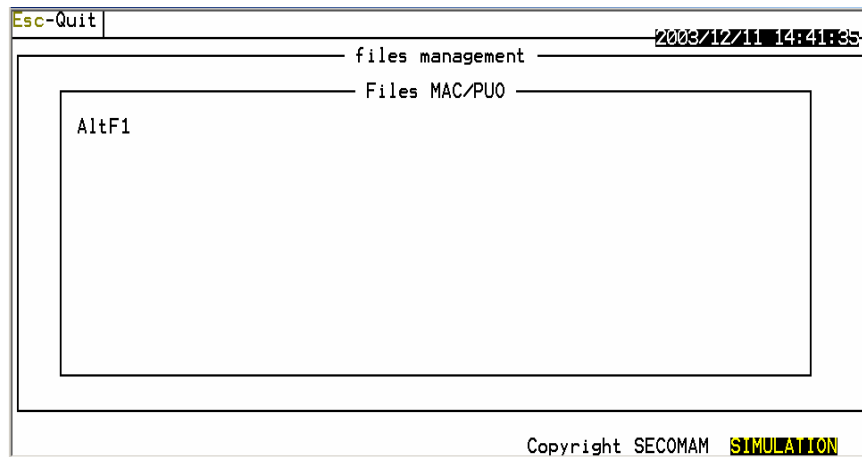
Choose the drive number as above.

Drive number: Define the type of drive in which the file(s) to be displayed can be found.

- A : floppy disk drive
- C : hard disk



When the parameters are defined, confirm.

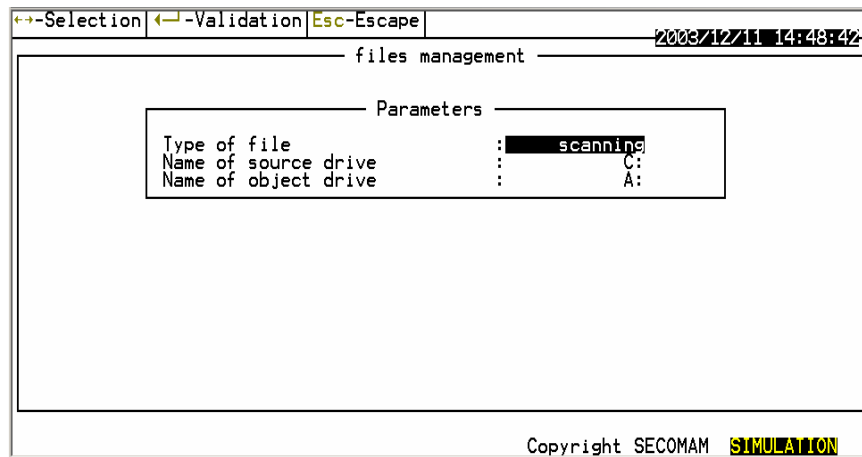


Example: List of "MACRO" files in hard disk C.

17.2.2 Save

This function allows to copy files from one drive to another. It is especially useful for saving curves or programs or for loading curves or programs into Uvi light (improved capabilities of spectrophotometer, spectra libraries, software updating,...).

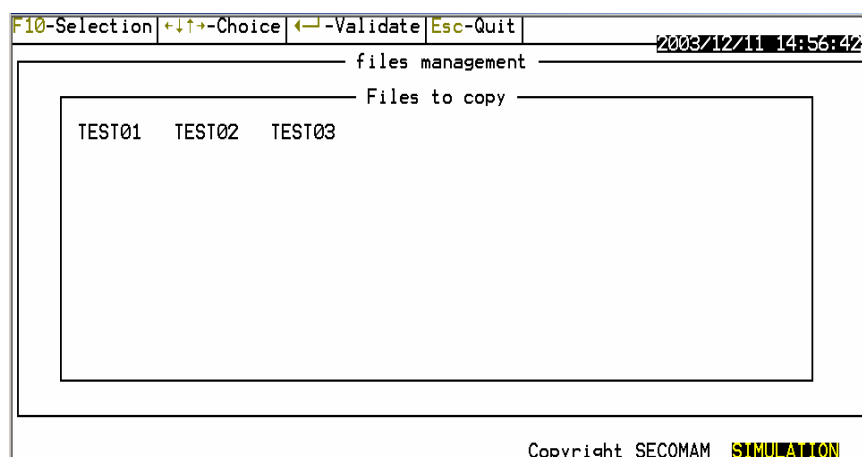
Press **F2 (Save)**.



Type of file: Select the types of file to be copied by means of the ← and → keys. Confirm.

Number of source drive: Select by means of the ← and → keys the type of drive (A, C) which includes the file to be copied.

Number of object drive: Select as above the type of drive (A, C) into which the selected file will be copied. When the parameters have been defined, confirm.



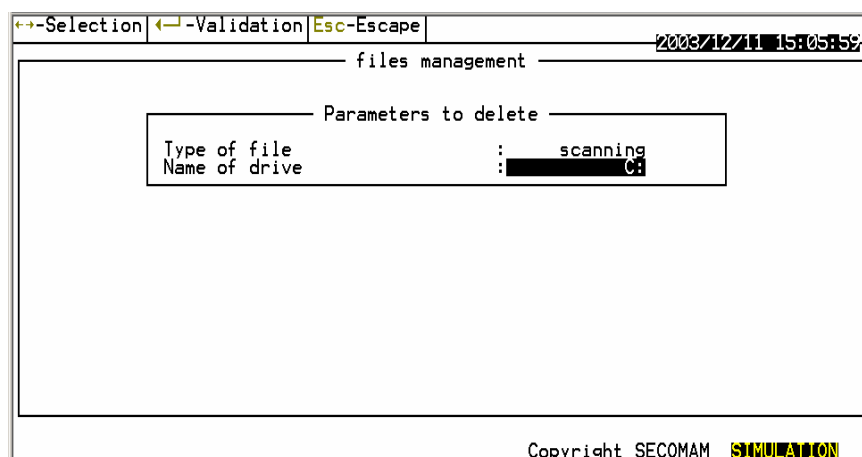
Select the files to be copied. Confirm and confirm.
When the copy is completed, the software returns to the file management menu.

17.2.3 Erase

This function allows to delete files (spectra, kinetic, ASCII, editor, macro or program files).

ALWAYS CHECK IF THE FILE TO BE DELETED IS THE RIGHT ONE.

Enter **F3 (Erase)**.



Type of file: with the ← and → keys, search for the type of file to be deleted (editor, program, ASCII, macro, spectra or kinetic file). Confirm.

Number of drive: define as above the type of drive (A, C) where the file to be deleted can be found. Confirm.

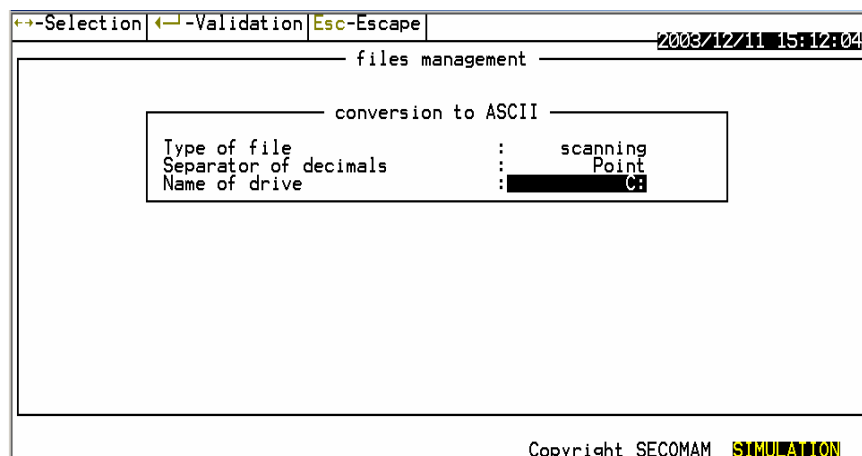
Select the files to be deleted.
Confirm. The files selected will be deleted.

When deletion is completed, the software returns to the file management menu.

17.2.4 Curves transformation in ASCII files

This function allows to use the data obtained with Uvi Light in another software.
For example, it is possible to transfer the data of a curve file (spectra or kinetic file) to a spreadsheet (ex.: Excel, ...) to run them.

Press **F4 (Curve → ASCII)**. The display is:



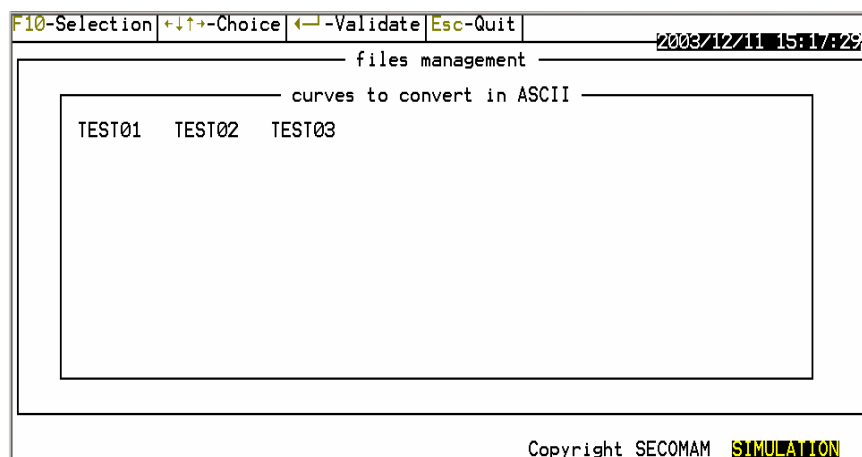
Type of file: with the ← and → keys, select the type of file to be converted (spectra or kinetic file). Confirm.

Decimal separator: point or comma.

In fact, if the values obtained (ex.: in a spectrum, wavelength and absorbance) have decimals, the type of separator must be set forth. A number of softwares into which the data will be transferred only accept one form of results:

The Uvi Light allows to adapt the files in order that they may be compatible with programs likely to receive them. Select as above the decimal point or the comma. Confirm.

Drive number: Precise the type of drive (A, C,) in which the file to be converted can be found. Confirm.



Select the file to be converted into ASCII. Confirm and confirm.

When conversion is completed, the software returns to the file management menu.

18 METROLOGY

18.1 VERIFICATION TEST

- Background noise verification.
- Straight light at 340 nm verification.
- Measure stability verification.
- Wavelength verification.
- Absorbance verification.

18.2 GENERALITY

Verification tests are the same for **Uvi Light XS**, **Uvi Light XT Dimension**, **Uvi Light PC**

18.3 STARTUP

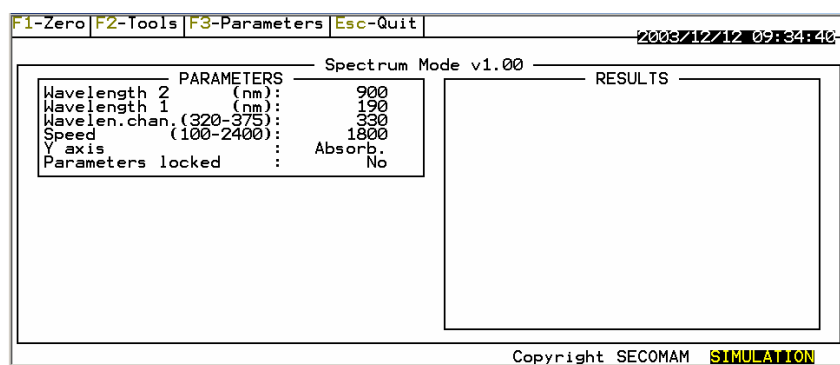
- Remove cuvette (if there is one) out of the cuvette holder.
- Switch the spectrophotometer on.
- Wait 45 minutes (Warm up).
- Press **F1 (Configuration)**. Select « **No** » for the « **Option** » parameter (working in monocell mode)

18.4 PERIODICITY

Verification tests are made once per year regularly, or every time the operator wants to be sure that the instrument is working well.

18.5 BACKGROUND NOISE VERIFICATION ON THE COMPLETE WAVELENGTH RANGE.

- Enter in spectrum mode.
- Enter parameters as follows:



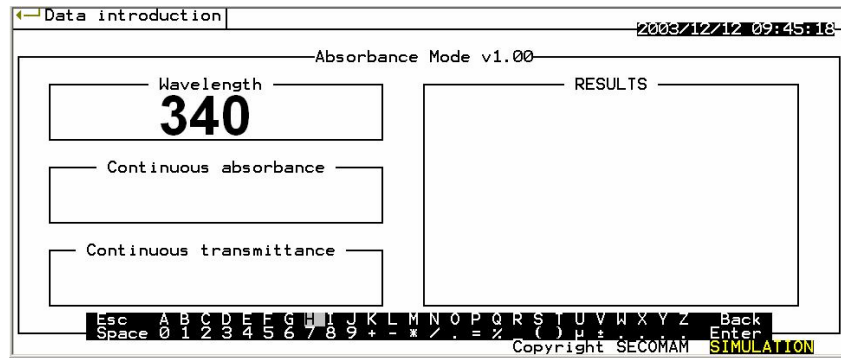
- Perform baseline (zero) on the air.
- Stopped the beam with opaque material.
- Launch the measure.

Results

Absorbance from 190 to 900 nm : > 2.5

18.6 STRAIGHT LIGHT VERIFICATION AT 340 NM

- Enter in the absorbance mode.
- Select 340 nm.



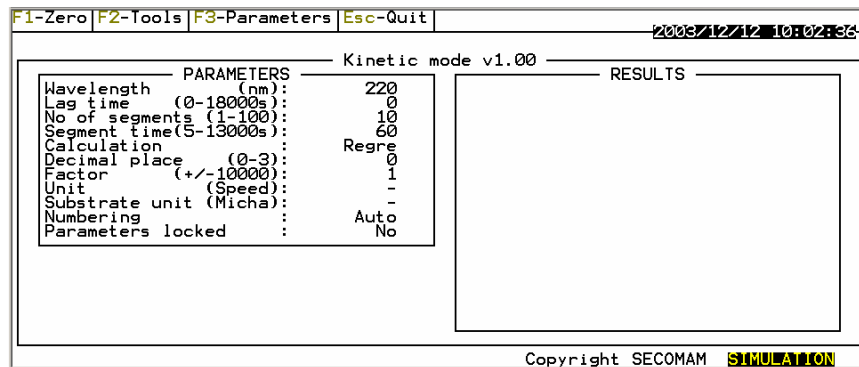
- Perform the zero on the air.
- Insert SCHOTT INSTRUMENTS standard filter (ref: 404686).
- Read the value.

Results

Absorbance at 340 nm : > 2.5 Abs

18.7 VERIFICATION OF MEASURE STABILITY

- Enter in kinetic mode.
- Enter parameters as follows:



- Perform the zero on the air.
- Launch the measure on the air.
- Make a zoom closer to the curve.
- Read the highest and the lowest absorbance value.
- Do again this operation with wavelength 340 nm.

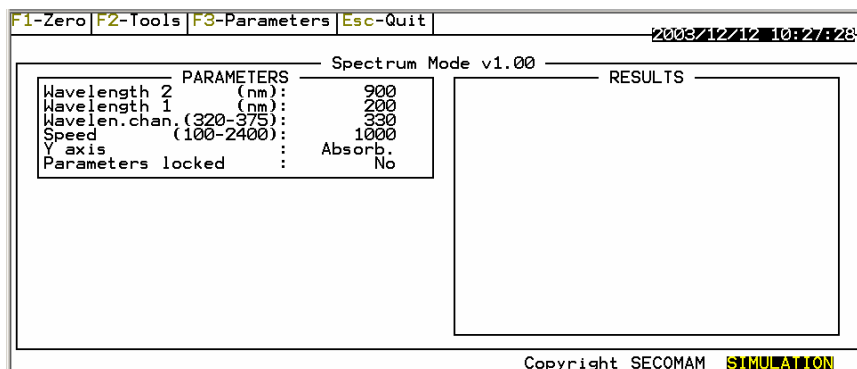
Results

- Estimate this gap and verify if the absorbance value (0.000) is included inside.

W.L. 220 nm	Tolerance on the entire kinetic: +/- 0.005 Abs
W.L. 340 nm	Tolerance on the entire kinetic: +/- 0.005 Abs

18.8 WAVELENGTH VERIFICATION

- Enter in the spectrum mode.
- Enter the parameters as follows:



- Perform baseline on the air.
- Measure the spectrum of holmium perchlorate solution (ref: 406817).
- Make an automatic reading of absorption picks.
- Compare theoretical picks and reading picks.

Results

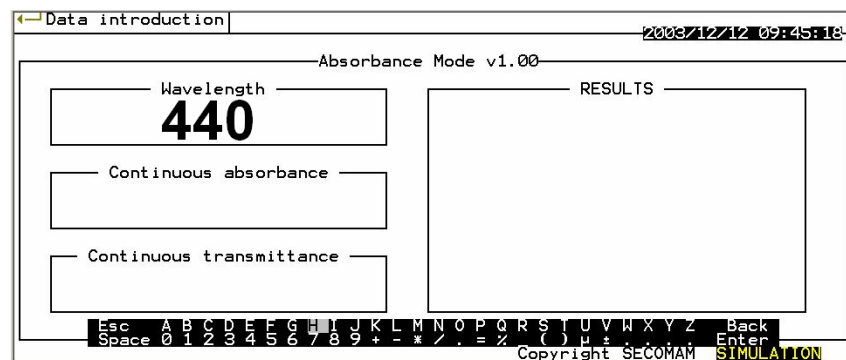
- Verify if the reading wavelengths of the holmium solution picks are included between the maximal and minimal theoretical picks values of this solution.

Uvi Light (5 nm band pass)	
Minimal W.L. (nm)	Maximal W.L. (nm)
239.7	241.9
286.7	288.9
360.0	362.2
536.9	538.7

Uvi Light (2 nm band pass)	
Minimal W.L. (nm)	Maximal W.L. (nm)
240.1	242.3
286.4	288.6
360.0	362.2
536.9	538.9

18.9 ABSORBANCE VERIFICATION

- Enter in absorbance mode.
- Select 340 nm.



- Perform zero on the air.
- Insert F2 filter (Set of secondary calibration filters ref: 0G6349).in the cuvette holder.
- Read the value.
- Insert standard filter F3, then standard filter F4.
- Read the values.
- Do again same operation at 465nm, 546 nm, 590 nm, and 635 nm.

Results

- Verify that the reading absorbances of standard filters F2, F3, F4 are included in the tolerance gap expressed as follows:

(Theoretical value* of std filter Fx – Tolerance) < Reading value of std filter Fx < (Theoretical value* of std filter Fx + Tolerance)

* Theoretical values of standard filters are given with every standard filters kit.

<i>FILTERS</i>	<i>FILTER F2</i>	<i>FILTER F3</i>	<i>FILTER F4</i>
W.L. (nm)			
440	Theoretical V. +/- 0.007 Abs.	Theoretical V. +/- 0.010 Abs.	Theoretical V. +/- 0.010 Abs.
465	Theoretical V. +/- 0.007 Abs.	Theoretical V. +/- 0.010 Abs.	Theoretical V. +/- 0.010 Abs.
546	Theoretical V. +/- 0.007 Abs.	Theoretical V. +/- 0.010 Abs.	Theoretical V. +/- 0.010 Abs.
590	Theoretical V. +/- 0.007 Abs.	Theoretical V. +/- 0.010 Abs.	Theoretical V. +/- 0.010 Abs.
635	Theoretical V. +/- 0.007 Abs.	Theoretical V. +/- 0.010 Abs.	Theoretical V. +/- 0.010 Abs.

18.10 SUMMARY TABLE

BACKGROUND NOISE VERIFICATION ON THE COMPLETE WAVELENGTH RANGE

Tolerance : > 2.5 Abs	
-----------------------	--

STRAIGHT LIGHT VERIFICATION AT 340 NM

Tolerance : > 2.5 Abs	
-----------------------	--

VERIFICATION OF MEASURE STABILITY

W.L. 220 nm	Toler. : +/- 0.005 Abs	
-------------	------------------------	--

W.L. 340 nm	Toler. : +/- 0.005 Abs	
-------------	------------------------	--

WAVELENGTH VERIFICATION

<i>Uvi Light (Band pass 5 nm)</i>			<i>Uvi Light (Band pass 2 nm)</i>		
Min. W.L. (nm)	Reading W.L.	Max. W.L. (nm)	Min. W.L. (nm)	Reading W.L.	Max. W.L. (nm)
239.7		241.9	240.1		242.3
286.7		288.9	286.4		288.6
360.0		362.2	360.0		362.2
536.9		538.7	536.9		538.9

ABSORBANCE VERIFICATION

<i>FILTERS</i>	<i>F2 FILTER</i> <i>Tolerance: +/- 0.007 Abs</i>		<i>F3 FILTER</i> <i>Tolerance: +/-0.010 Abs</i>		<i>F4 FILTER</i> <i>Tolerance: +/-0.010 Abs</i>	
	Theoretical V.	Reading value	Theoretical V.	Reading value	Theoretical V.	Reading value
440						
465						
546						
590						
635						

19 MAINTENANCE

The spectrophotometer does not require any specific maintenance (Only the halogen lamp or the deuterium lamp must be changed by the user). However, the spectrophotometer must be kept perfectly clean, in particular the cell compartment which must not contain any spilt chemicals; the input and output windows of the light beam, in the cell compartment, must be cleaned regularly with a non fluffy cloth.

To change the deuterium lamp or halogen lamp, see installation guide (REF: 0M8039).

The operator will find here under some probable causes of troubles and some advices to help him to solve these troubles. For any no solved problem, call SCHOTT INSTRUMENTS or technicians approved by SCHOTT INSTRUMENTS.

The spectrophotometer does not perform the zero

EXPLANATION
The photocell does not receive enough energy
SOLUTION
Verify that: - the lamp used is still working, if not change it, - if the measure is performed in UV light(190-330 nm), the cuvette is built in quartz (QS is written on its side), - the cuvette is installed in the right direction, - the optical sides of the cuvette are perfectly clean, - the distance between the centre of measuring windows (when a flow through cell is used) and the bottom of the cuvette is 8,5 mm, - if there are no bubbles or impurities which block the beam, - if the date beyond which the reagent is not to be used, is not over passed - If the blank or reference solution (reagent) is pure or conform to its use.

There are some problems during printing

EXPLANATION
The printer does not receive any data from Uvi Light spectrophotometer.
SOLUTION
Verify that : - the printer is connected to the main, - the printer used is a parallel printer, - the used cable is the correct one (SCHOTT INSTRUMENTS reference: 0J5706), - the cable is correctly connected on the printer and on the spectrophotometer (tighten the screws connector) - the standard of the selected printer corresponds to the used printer)

The absorbance is too high

EXPLANATION
Something blocks the beam or there is no beam.
SOLUTION
Verify that : - the cuvette is setting in the correct position, - bubbles and impurities does not block the beam, - selected lamp is working properly.

The absorbance is negative

EXPLANATION The absorbance of solution used to perform the zero is higher than the sample absorbance.
SOLUTION Verify that : - the absorbance of solution used to perform the zero is not too high, - there are no bubbles or impurities inside blank solution.

Results instabilities

EXPLANATION The lamp used still functions but must be close to its end of lifetime. The sample is not stable or too concentrated.
SOLUTION Change the lamp used. Verify that: - absorbance of the reference solution is not too high, - the sample is stable, - sample concentration is not too high, - there are not bubbles or impurities.

The spectrophotometer does not do anything any more

EXPLANATION The instrument can be carrying out a calculation or a no locatable operation by the user
SOLUTION Wait a minute If after one minute the instrument does not do anything any more, switch it off and on and re start it again.

Wavelength abnormalities

It is easy to check if the spectrophotometer is well adjusted as a whole in regards to the wavelength.

- Select absorbance mode.
- Check with a sheet of white paper in the cell well the correspondence of the colors with the wavelengths:

650 nm - red
600 nm - orange.
578 nm - yellow.
547 nm - green.
500 nm – turquoise blue.
450 nm - blue.
400 nm - purple.

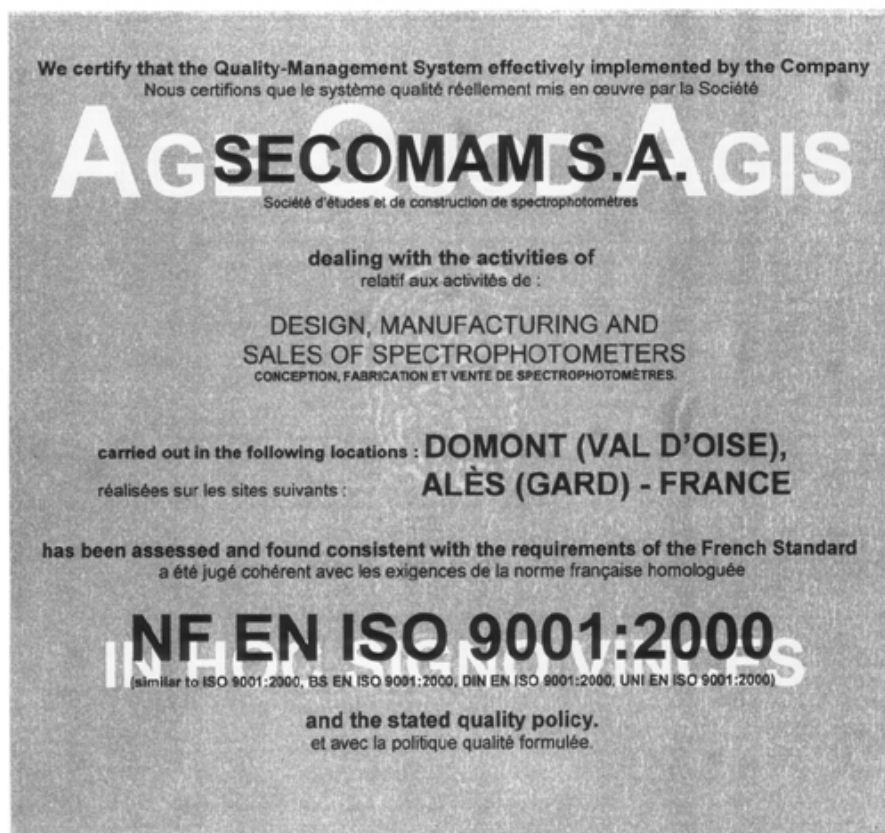
20 ISO 9001 CERTIFICATE

Unite with quality !



Bau auf Qualität !

CERTIFICAT



Lyon, April 3rd, 2003

The Management Representative
Le Représentant de la Direction
Monsieur Guy MANCEL

The President and Managing Director
Monsieur Daniel CONSTANT
Le PDG de l'Entreprise certifiée

This certificate N° 2003-CLXV. is valid according to the associated contract, until April 2nd, 2006.



N° 4-016/98



The President
of the Certification Committee
Le Président du Comité de Certification

Adjoins-Toi la qualité !

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